

STIC-Biotech/ChemLib

86436

From: McElwain, Elizabeth
Sent: Tuesday, February 11, 2003 10:48 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Please search for prior art and for interference:

09/883,797 - for DNA encoding SEQ ID NO: 2.

Thank you,
Beth

Elizabeth F. McElwain, Ph.D.
U.S. Patent and Trademark Office
Tech Center 1600, Art Unit 1638
room CM1-9E11
mailbox CM1-9E12
703-308-1794
elizabeth.mcelwain@uspto.gov

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

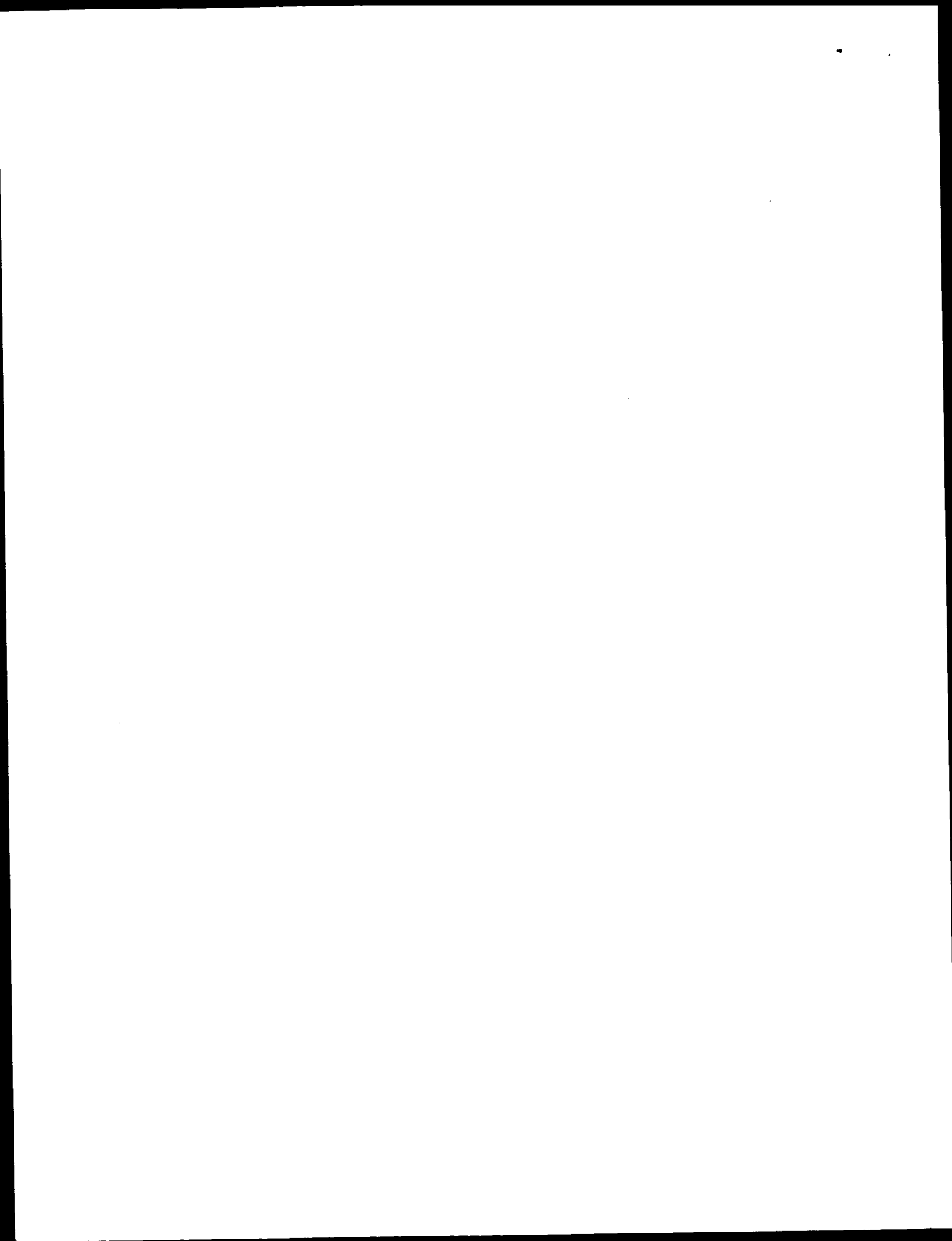
Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 2/14
Date Completed: 2/20
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 08:33:57 : Search time 3473 Seconds
(without alignments)
4357.460 Million cell updates/sec

Title: US-09-883-797-2

Perfect score: 2680

Sequence: 1 MDRRLTAEMAFRDSSSAVI.....EMTGNWAGSIDQYFVKVQ 520

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n_model -DEV=xlp
-O=/cgn2.1/USPTO.spool/US09883797/runat_14022003_102501_19502/app_query.fasta_1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09883797.@cgn.1.1.3745.@runat_14022003_102501_19502 -NCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_un:*
28: em_uni:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2680	100.0	1560	6	AR174886 Sequence
2	2680	100.0	1563	6	AX12586 Sequence
3	2680	100.0	1563	8	AF053345 Arabidops
4	2680	100.0	1618	8	AY096568 Arabidops
5	2680	100.0	1896	8	AY074285 Arabidops
6	2680	100.0	86436	8	AC007323 Genomic s
7	2020.5	75.4	127990	8	AF004939 Lotus jap
8	1764	65.8	1929	8	AF082033 Hemerocal
9	1720.5	64.2	131142	8	AC129008 Genomic s
10	1679	62.6	139914	2	AP003623 Oryza sat
11	1674.5	62.5	119028	2	AC098832 Oryza sat
12	1658	61.9	2018	8	ZMA292770 Zea mays
13	1639	61.2	95167	8	AC003105 Arabidops
14	1626	60.7	1803	8	AF424620 Arabidops
15	1626	60.7	1845	8	AY035030 Arabidops
16	1608	60.0	1807	8	AF247134 Limnanthe
17	1595.5	59.5	2143	6	AX155071 Sequence
18	1581.5	59.1	203125	2	AC120986 Oryza sat
19	1574	58.7	144359	8	AC087723 Oryza sat
20	1563	58.3	1548	8	AR174892 Sequence
21	1563	58.3	120977	8	AC025808 Genomic s
22	1559.5	58.2	178025	2	AP005008 Oryza sat
23	1531.5	57.1	1611	6	AR174890 Sequence
24	1531.5	57.1	114418	8	AC007047 Arabidops
25	1525.5	56.9	1765	8	AY082610 Tropaeolu
26	1525.5	56.9	1765	8	AY082610 Tropaeolu
27	1521.5	56.8	1812	8	SCU37088 Simmondsia
28	1519.5	56.7	1783	6	II4085 Sequence 11
29	1519.5	56.7	1783	6	II4085 Sequence 3
30	1513.5	56.5	1819	8	AY089012 Arabidops
31	1505	56.2	5600	8	AF188485 Arabidops
32	1505	56.2	55870	8	AC005819 Arabidops
33	1497	55.9	1733	6	II4084 Sequence 10
34	1497	55.9	1733	6	II4084 Sequence 2
35	1472	54.9	1903	8	AY072823 Gossypium
36	1468.5	54.8	87937	8	ATAC009400 Arabidops
37	1443.5	53.9	87286	6	AB026651 Arabidops
38	1441	53.8	1650	6	AR174889 Sequence
39	1438.5	53.7	1491	6	AR165358 Sequence
40	1438.5	53.7	1502	6	AR174891 Sequence
41	1438.5	53.7	1807	6	AR165357 Sequence
42	1438.5	53.7	1827	8	AY087518 Arabidops
43	1438.5	53.7	1829	8	AF129511 Arabidops
44	1438.5	53.7	3722	6	AR165356 Sequence
45	1438	53.7	1911	8	AY039563 Arabidops

ALIGNMENTS

RESULT 1

AUTHORS

Glazebrook, J., Wang, X., Dangl, J.L., Bulgem, T. and Zhu, T.
 TITLE plant genes, the expression of which are altered by pathogen infection

JOURNAL

Patent: WO 0222675-A 350 21-MAR-2002;
 Syngenta Participations AG (CH); UNIVERSITY OF NORTH CAROLINA AT
 CHAPEL HILL (US); Glazebrook, Jan (US); Wang, Xun (US); Dangl,
 Jeffrey L. (US); Bulgem, Thomas (US)

FEATURES

Location/Qualifiers
 1..1563
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"

BASE COUNT

421 a 355 c 379 g 408 t

ORIGIN

Alignment Scores:

Pred. No.: 2..le-240 Length: 1563
 Score: 2680.00 Matches: 520
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-883-797-2 (1-520) x AX412586 (1-1563)

QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValIle 20
 Db 1 ATGATCGAGAGAGATTAAACGGCGAGATGCGTTTCGAGATTTCATCATCGCGCTTATA 60
 QY 21 ArgIleArgArgGluProAspLeuThrSerValLysLeuLysTyrValLysLeu 40
 Db 61 AGAATTCGAAGACGTTTGCGCGATTATTAACGTCGCTTAAGCTCAATACGTGAAGCTT 120
 QY 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeu 60
 Db 121 GGACTTCACAACTCTTGCAAGCGTACACCATCTCTCTTCTTAAATATTCCTCCCTTA 180
 QY 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80
 Db 181 ACCGGAAACCGTGTGGTTCAGCTAACCGGTCTAACGTTTCGATCGTCTCTGAGCTTTGG 240
 QY 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100
 Db 241 TCTAACCGCGGTTTCAACTCGACACGGCAGACTTACCTGCTTGGTTTCTCTCCCTCC 300
 QY 101 PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSer 120
 Db 301 TTCGTTTTCACCTCTACCTGGCTAAACCGGTCTAAACCGGTTTACCTAGTGGATTCTCC 360
 QY 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140
 Db 361 TGCTACAAACCGAAGACAGCGTAAATATCATGATAGATTCGTTCTTGACGATCAGCTGAG 420
 QY 141 GluAsnGlySerPheThrAspThrValGlnPheGlnArgIleSerAsnArgAla 160
 Db 421 GAAATGGATCATTCACCGATGACACGGTTTCAAGTCCAGCAAGATCTCGAACCGGGCC 480
 QY 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsn 180
 Db 481 GGTGTGGGAGACGACGATCTCGCACGTGGCATAAATCTCAACGCCCGCGAAGCTTAAAT 540
 QY 181 MetSerGluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhePhe 200
 Db 541 ATGTCAGAGGACGTCGCGAAGCTGAAGCCGTATGTTTGGAGCCCTAGATTCCTCTTC 600
 QY 201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
 Db 601 GAGAAACCGGAATTAACCGCGCGAAGTCGGAATCTTGATAGTAAACTGCAGCTTATTC 660
 QY 221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
 Db 661 AATCCGAGCGGCTCTATACAGCATGATCGTGAACCATTAAGATGAGAGAAGACATC 720
 QY 241 LysSerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla 260

Db 721 AAAAGTTACACCTCGGAGGAATGGTTGCTCCGCCGGAATTAATCTCAATCGATCTCGCT 780
 QY 261 AsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValValSerThrGluAsnIle 280
 Db 781 AACAAATCTCTCAAGCAAAACCCATAATCTTACGCTGCTGCTGGTAAGCACGGAACATA 840
 QY 281 ThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg 300
 Db 841 ACCCTAAACCTGGTACTTCGGAATGACCGGTCATCTCTCTGCAACTGCATCTTCCGA 900
 QY 301 MetGlyGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyr 320
 Db 901 ATGGCGGAGCTGCGATTCTCTCTTAACCGCGCTCAAGACCGGAAGAAAGTCAAGTAC 960
 QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
 Db 961 TCCTGTGTCAACCTGCTTCGAACACATAAAGGATCAGACGACAGCAACTACATTTGCGTG 1020
 QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
 Db 1021 TACCAGAAGGAGACGAGAGAGGAACAATCGGTCTCTTTAGCTAGAGAGCTCATGTCT 1080
 QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeu 380
 Db 1081 GTCCCGGAGACGCTCTGAAAAACAACATCAGCACTTTAGACCGCATGGTTCTTCCATTG 1140
 QY 381 SerGluLysLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
 Db 1141 TCAGACGATGTGATGTTCTTGTATTTCTTGTCAAAAGGAAGATGTTCAAGTTAAAGTT 1200
 QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
 Db 1201 AAACCGTATATTCGCGATTTCAGCTAGCTTTCGAGCATTTCTGTATTCACGAGGAGGT 1260
 QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLysAspTrpHisMetGluPro 440
 Db 1261 AGAGCGGTTCTAGACGAAGTGCAGAAAGATCTTGATCTCAAGATTCGCACATGGAACCT 1320
 QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrTrpGluMet 460
 Db 1321 TCTAGAATGACTTTCACAGATTTCGTAACACTTCGATAGCTGCGCTTTGGTAGAGATG 1380
 QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
 Db 1381 GCTTATACCGAAGCTTAAGGTCGGTTAAAGCTGAGTGGTACCGACTTTGGCAGATTGCGTT 1440
 QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
 Db 1441 GGATCGGGTTTCAAGTGTAAATAGTCGGTTTGAAGCGTTTACGACCGGTTTCGACGGAG 1500
 QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValGln 520
 Db 1501 GAGATGACCGGTAATGCTTGGGCTGTTGATTCATATCCGGTTAAAGTTTGTGCA 1560
 RESULT 3
 AF053345 1563 bp DNA linear PLN 20-OCT-2000
 LOCUS Arabidopsis thaliana fatty acid elongase 3-ketoacyl-CoA synthase 1
 DEFINITION (KCS1) gene, complete cds.
 ACCESSION AF053345
 VERSION AF053345.1 GI:4091809
 KEYWORDS
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 1563)
 Todd, J., Post-Beitemmiller, D. and Jaworski, J.G.
 KCS1 encodes a fatty acid elongase 3-ketoacyl-CoA synthase
 affecting wax biosynthesis in Arabidopsis thaliana
 Plant J. 17 (2), 119-130 (1999)

Thu Feb 20 11:03:33 2003

```

MEDLINE      99174280
PUBMED       10074711
REFERENCE    2 (bases 1 to 1563)
AUTHORS      Todd,J.F., Post-Reittenmiller,M. and Jaworski,J.G.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAR-1998) Chemistry and Biochemistry, Miami
              University, Oxford, OH 45056, USA
FEATURES
  source
    1..1563
      /organism="Arabidopsis thaliana"
      /cultivar="Columbia"
      /db_xref="taxon:3702"
      /chromosome="1"
      /map="YAC yUP2001"
    1..1563
      /gene="KCS1"
    1..1563
      /gene="KCS1"
      /function="involved in wax biosynthesis"
      /note="condensing enzyme"
      /codon_start=1
      /product="fatty acid elongase 3-ketoacyl-CoA synthase 1"
      /protein_id="AAC99312.1"
      /db_xref="GI:4091810"
      /translation="MDREKLTAEMAPRDSASVIRIRRLPDLITSVKLYVKLGLHN
        SCNVITLFLILPLTGLVQLTGLTDFSELNSQAVQLDITATRLCLFLSFV
        LTVYANRKNPVYVDFSCYKPEDERKISVDFLTMEENGSTFDDPQFOQRISNR
        GLGDEYLPGRITSTPKLNMSEARAEAVMFGALDLSFEKTKRPAEYGLIVNCS
        LNPSTLSAMIVNHVKMRDIDKSYNLGCMGCSAGLISIDLANNLLKANPNSAVVYS
        TENITLWFGNDRSMILLNCIFRMGGAALLSNRRDRKSKYSLVNVVTRHKGSDD
        KNYVYQDEDEGTIGVSLARELMSVAGDALKNTITLGPVPLPLSEOLMFLISLVK
        RMFKLVKPYIPDFKLAHFHFCIHAGRAVLDEVKANLWLKWHMPSRMTLHREGN
        TSSSLWYEMAYTEAKRGVKAGRLWQIAPGSGFKNSAVMKALRPVSTEMTGNANA
        GSIDQYPVKVVQ"
BASE COUNT  421 a 355 c 379 g 408 t
ORIGIN
Alignment Scores:
Pred. No.:      2,1e-240      Length:      1563
Score:          2680.00      Matches:      520
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              8              Gaps:        0

US-09-883-797-2 (1-520) x AF053345 (1-1563)
QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerSerAlaValIle 20
Db 1 ATGGATCGAGAGAGATTAAAGCGGAGATGGCGTTTCGAGATTTCATCATCGGCGGTATA 60
QY 21 ArgIleArgArgArgLeuProAspLeuThrSerValLysLeuLysTyrValLysLeu 40
Db 61 AGAATTCGAAGACGTTTCGCGGATTATTAAAGCTCGGTTAAAGCTCAAAATACGTGAAGCTT 120
QY 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeu 60
Db 121 GGACTTCACAACTCTTCGCAACGTGACCACCATCTCTTCTTCTTAATTATCTCTCTTTA 180
QY 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80
Db 181 ACCGGAACCGTGTGTTGAGTAAACCGGTCTAACGTTTCGATACGTTCTCTGAGCTTTGG 240
QY 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100
Db 241 TCTAACCGCGGTTCACACTCGACGCGGACGAGACTTACCTGCTTGTGTTTCTCTCTCC 300
QY 101 PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSer 120
Db 301 TTCGTTTTCACCTCTACGTGGTAAACCGGTCTAAACCGGTTCACCTAGTGGATTCTCC 360
QY 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140

```

```

361 TGCTACAAACCGGAAGACGACGCTAAAATATACAGTAGATTCTGTTTGTGACGATGACTGAG 420
141 GluAsnGlySerPheThrAspAspThrValGlnPheGlnGlnArgIleSerAsnArgAla 160
421 GAAATGGATCATTCACCGCATGACACGGTTTCAAGTTCACGAAGAATCTCGAACCGGGCC 480
161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsn 180
481 GGTTTGGGAGACGAGACGATATCTCCACGTGGCATAAATCTCAACGCCGCCGGAAGCTAAAT 540
181 MetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe 200
541 ATGTCAGAGGACGTCGCGGAGCTGAAGCCGTATGTTTGGAGCCCTAGATTCCCTCTTC 600
201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
601 GAGAAACCGGAATTAACCGGCCGGAAGTCGGAATCTTATGATAGTAACCTGACGCTTATTC 660
221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
661 AATCGACGCGCTCTCTATCAGCGATGATCGTGAACCATTTACAAGATGAGAGAGACATC 720
241 LysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla 260
721 AAAAGTTACAACTCGGAGAAATGGGTGCTCCGCCGGAATTAATCTCAATCGATCTCGCT 780
261 AsnAsnLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIle 280
781 AACAATCTCTCAACCAACCCCTAATCTTACGCTGCTGCTGGTAAAGCAGGAAACATA 840
281 ThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg 300
841 ACCCTAACTGGTACTTCGGAATGACCGGTCAATGCTCTCTGCAACTGCTCATCTTCGGA 900
301 MetGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyr 320
901 ATGGCGGAGCTCGGATCTCTCTCTTAACCGCGCTCAAGACCGGAAGAGTCAAGATAC 960
321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
961 TCGCTGGTCAACGTCGTTTCAACACATATAAGGATCAGACGACAAAGAACTACAATTGCGTG 1020
341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
1021 TACCAGAAGGAGACGAGAGAGAGAACAAATCGGTGCTCTTTAGCTAGAGAGCTCATGCT 1080
361 ValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyPrometValLeuProLeu 380
1081 GTCGCGGAGACGCTCTGAAACCAACATCACAGCTTTTAGGACCGATGGTTCTTCCATTG 1140
381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
1141 TCAGAGCAGTGTGATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
1201 AAACCGTATATTCGCGATTTCAAGCTAGCTTTTCGAGCATTTCTGTATTTCACGAGAGGT 1260
421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluPro 440
1261 AGAGCGGTTCTAGACGAAGTGCAGAAATCTTGTATCTCAAAAGATTGGCACATGGAACCT 1320
441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerSerLeuTrpTyrGluMet 460
1321 TCTAGAATGACTTTGCACAGATTTCGTAACACTTCGAGTAGCTCGCTTTTGGTATGATGATG 1380
461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
1381 GCTTATACCGAAGCTAAGGTCGGGTAAAGCTGTTGACCGACTTTTGGCAGATTTGCGTTT 1440
481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
1441 GGATCGGTTTCAAGTGTAAATAGTCGGGTTTGGAAAGCGTTACGACCGGTTTTCACGCGAG 1500

```

Qy 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValValGln 520
 |||||
 Db 1501 GAGATGACCGGTAATGCTGGGCTGGTTGCGATTGATCAATATCCGGTTAAAGTTGTGCAA 1560

RESULT 4
 AY096568 1618 bp mRNA linear PLN 06-MAY-2002
 LOCUS
 DEFINITION Arabidopsis thaliana putative fatty acid elongase 3-ketoacyl-CoA
 synthase 1 (Atlg01120) mRNA, complete cds.
 AY096568
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana
 Arabidopsis thaliana
 Arabidopsis thaliana
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 1618)

REFERENCE
 AUTHORS
 Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
 Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
 Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
 Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.,
 Arabidopsis Open Reading Frame (ORF) Clones
 Unpublished

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 2 (bases 1 to 1618)
 Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
 Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
 Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
 Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.,
 Arabidopsis Open Reading Frame (ORF) Clones
 Unpublished

TITLE
 JOURNAL
 COMMENT
 Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 The RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA : "RIKEN
 Arabidopsis Full-Length cDNA"): Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and
 sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K.,
 Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
 Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
 Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
 Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
 Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
 Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
 to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP
 /PGEC) contributed equally to this work as pIs.

FEATURES
 source
 Location/Qualifiers
 1. .1618
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /chromosome="1"
 /clone="U19207"
 /note="This clone is in pUNI 51."
 ecotype: Columbia
 1. .1618
 /gene="Atlg01120"
 1. .1567
 /gene="Atlg01120"
 /codon_start=1
 /evidence=experimental

/product="putative fatty acid elongase 3-ketoacyl-CoA
 synthase 1"
 /protein_id="AAM20218.1"
 /db_xref="GI:2046593"
 /translation="MERTNSIEMDRERLTAEAFRDSSSAVIRPRRLPDLLTSVKKL
 YVKLGHSNVTILFELIPLTGLVLTGLTDTFSELNSQAVQIDTATRLT
 CLVFLSFVLTYVANRSKPYLVDFSCYKPDERRKISVDSFELTMTTEGSGFTDDTVQF
 QORISNRAGLGDETYLPRGITSTPPKLMSEARAEAEAFMGALDSLFKTKGKPAEV
 GILIVNSLENPTPSUSAMINVHYKREDIKSYNLGGMGCSAGLISIDLANNLLKANP
 NSYAVSTENITLNMVFGNDRSMCLNCIFRMGGAAILLSNRQDRKKSKYSLVNVV
 RTHKSDKNYCNVQKEDERTIGVSLARELMSVAGDALKTNTITLGPMLPLSEQL
 MFLISLVKRMFKLVKPYIPDFKLAFEHFCIHAGRAVLDEVKNDLQKDHMEPSR
 MTLHFRGNTSSSLIWTMEATKGRVKAGDRLWQIAFGSOFKCNASAVKALKALRPVSTE
 EMTGNWAGSIDQVPYKVVQ"
 1588..1618
 3'UTR
 /gene="Atlg01120"
 BASE COUNT 442 a 361 c 392 g 423 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2-21e-240 Length: 1618
 Score: 2680.00 Matches: 520
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-09-883-797-2 (1-520) x AY096568 (1-1618)
 Qy 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValile 20
 |||||
 Db 25 ATGGATCGAGAGAGATTAAACGGCGAGATGGCGTTTCGAGATTTCATCATCGCGGTATA 84
 Qy 21 ArgIleArgArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeu 40
 |||||
 Db 85 AGAATTCGAAGACGTTTGGCGGATTATTAAACGTCGTTAAAGCTCAAAATACGTGAAGCTT 144
 Qy 41 GlyLeuHisAsnSerCysAsnValThrIleLeuPhePheLeuIleLeuProLeu 60
 |||||
 Db 145 GGACTTCACAACTTGGCAACGTGACACGAGACTTTCCTCTCTTAATATTCTTCCTTA 204
 Qy 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80
 |||||
 Db 205 ACCGGAACCGTGCTGGTTCAGCTAACCGGTCCTAACCGTTCGATACGTTCTCTGAGCTTGG 264
 Qy 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100
 |||||
 Db 265 TCTAACACGCGGTTTCAACTCGACACGCGCAGAGACTTACCTGCTTGGTTTTCCTCC 324
 Qy 101 PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSer 120
 |||||
 Db 325 TTCGTTTGACCCCTCTAGCTGGCTAACCGGCTAAACCGGTTTACCTAGTGGATTTCTCC 384
 Qy 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140
 |||||
 Db 385 TGCTACAAACCGGAAGACGAGCGTAAATAATATCAGTAGATTTCGTTCTTGACGATGACTGAG 444
 Qy 141 GluAsnGlySerPheThrAspAspThrValGlnPheGlnArgIleSerAsnArgAla 160
 |||||
 Db 445 GAAATGGATCATTCACCGATGACACGGTTTCAGTTCCAGCAAGAAATCTCGAACCGGGCC 504
 Qy 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsn 180
 |||||
 Db 505 GGTTTGGAGACGAGAGCTATCTGCCACGTGGCATACTTCACGCCGCCGGAAGCTAAAT 564
 Qy 181 MetSerGluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe 200
 |||||
 Db 565 ATGTCAGAGCACGTCGCCGAAGCTGAAGCCGTTATGTTTGGAGCCTTAGATTCCCTCTTC 624
 Qy 201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
 |||||
 Db 625 GAGAAACCCGGAATTAAACCGGGCGAAGTCGGAATCTTGTAGTAAATGACGCTTATTC 684

Thu Feb 20 11:03:33 2003

REFERENCE	1 (bases 1 to 1896)	Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
JOURNAL	Arabidopsis Full Length cDNA Clones	
REFERENCE	2 (bases 1 to 1896)	Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
JOURNAL	Direct Submission	
REFERENCE	Submitted (11-JAN-2002)	Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
AUTHORS	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.	
TITLE	The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.	
JOURNAL	Yamada,K. (SSP/PGECC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and theologis,A. (SSP/PGECC) contributed equally to this work as PIs.	
COMMENT	Location/Qualifiers	
FEATURES	1..1896	/organism="Arabidopsis thaliana"
source	/db_xref="taxon:3702"	
	/chromosome="1"	
	/clone="RAFL09-59-C06 (R19207)"	
	/note="This clone is in a modified pBluescript vector (F1C-1) as a BamHI/XhoI insert."	
	ecotype: Columbia"	
gene	1..1896	
	/gene="Atlg01120"	
5'UTR	1..189	
	/gene="Atlg01120"	
	190..1776	
CDS	/gene="Atlg01120"	
	/codon_start=1	
	/evidence=experimental	
	/product="putative fatty acid elongase 3-ketoacyl-CoA synthase 1"	
	/protein_id="AA166982.1"	
	/db_xref="GI:18377664"	
	/translation="MERTNSIEMDRERLTAEAFRDSSAVIRRRRLDILLTSVKLK VVKGLHNSCNVTTLFLIILPTGLTVQLTDFITSELWSNQAVQLDTATRLT QFLSVLTLTVANRSPKPYLVDVSCYPEDERRIKSVDSFLTMTEENGVSFTDDTVQF QOIRNSRAGLDGTYLPRGITSTPPKLNMSAEAAEAFMGALDLSLFKGTGKPAEV GILLVNGSLFNPSTLSIAIVNHYKMKRCDIKSYNLGGMCSAGLISDIANNLLKAN NSYAVVSTENITLTPGNDNRMLNCRIFPMGAAIILLNRRDRKSKYSLVNVP TRHKSDDKNTNCVQEDERGTIGVSLARELMSVAGDALKTNTITLGPMLPLPSOL MFLISLVKRMFKLWKPYIPDFKLAFEFCHTHAGGRAVLDEQNLDKDWMHPSR MTLHRFGNTSSSLVYEMAYTEAKGRVKGADRLWQIATFGSGFKCSAVWKALRPVSTE EMTGNWAGSIDQYPVKVVQ"	
	1777..1896	
	/gene="Atlg01120"	
3'UTR		

1 (bases 1 to 1896)

Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chang,E., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Kim,C., Lam,B., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Arabidopsis Full Length cDNA Clones

Unpublished

2 (bases 1 to 1896)

Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission

Submitted (11-JAN-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGE (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGE) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGE) contributed equally to this work as PIs.

Location/Qualifiers

1..1896

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/chromosome="1"

/clone="RAFL09-59-C06 (R19207)"

/note="This clone is in a modified pBluescript vector (FLC-1) as a BamHI/XhoI insert."

ecotype: Columbia"

1..1896

/gene="Atlg01120"

1..189

/gene="Atlg01120"

190..1776

/gene="Atlg01120"

/codon_start=1

/evidence=experimental

/product="putative fatty acid elongase 3-ketoacyl-CoA synthase 1"

/protein_id="AAL66982.1"

/db_xref="GI:18377664"

/translation="MERTNSIEMDRERLTAEAFRDSSAVIRIRRLPDLLTSVKLK VVKLGHSNVTTLFLFLLIPLVTGLTGLTFTDSELWSNQAVOLDTATRLT VVKLFLSVLTVANRSKPVYLVDFSCYKPEDERISVDFSLTMEENGSTDDTVQF QQRISNAGLGDETYLPRGITSTPKLMSAEAEAVMFGALDSLEKFTGKPAEV GILLVNCSEFNPTSLSNIVHYKMRDIIKSYNLGGMCSAGLISIDIANLLKANP NSAVVVSSTENITLNTWTFGNDRSMMLCNCIRMGGAAILNRRDOKRKSYSLVNV RTHKSDDDKNVCYQKEDERTIGVSLAREHMSVAGDAIKNTITLGPWLPISLQ MFLISLVKRRKMLKVPYIPDFLAFELFCIHAGLMDVDEYQNLDKADWMEPSR MTLHRFGNTSSSLWEMAYTEAKGRVKAGDRLQWIAFGSGFKNCNSVWKAIRPVSTE EMTCNWAGSIDQYVKVQV"

1777..1896

/gene="Atlg01120"

BASE COUNT	526 a	419 c	412 g	539 t
ORIGIN				

Alignment Scores:

Pred. No.:	2,76e-240	Length:	1896
Score:	2680.00	Matches:	520
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-09-883-797-2 (1-520) x AY074285 (1-1896)

QY	1	MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValLeu	20
Db	214	ATGGATTCAGAGAGATTAAACGCGAGATGGCGTTTCGAGATTCAATCGGCGGTATA	273
QY	21	ArgIleArgArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeu	40
Db	274	AGAAATTCGAACAGGTTTCGCCGATTAATAACGTCGGTTAAGCTCAAAACGTAAGCTT	333
QY	41	GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuLeuIleLeuProLeu	60
Db	334	GGACTTCACAACTCTTGCAACGTCGACCACTTCTCTCTCTTAAATTAATCTTCCTTAA	393
QY	61	ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTyr	80
Db	394	ACCGGAACCGTCGTGGTTTCAGCTAACCGGCTTAACGTTTCGATACGCTTCTCTCAGCTTTGG	453
QY	81	SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer	100
Db	454	TCTAAACAGCGGTTCAACTCGACACGCGAGAGACTTACTGCTTGGTTTTCCTCTCC	513
QY	101	PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSer	120
Db	514	TTCGTTTGGACCTCTACGTGGCTTAACCGGTTAAACCGGTTTACCTAGTGATTTCTCC	573
QY	121	CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu	140
Db	574	TGCTACAAACCGGAAGACGAGCGTAAATAATCAGTAGATTGTTCTTGACGATGACTCAG	633
QY	141	GluAsnGlySerPheThrAspAspThrValGlnPheGlnArgIleSerAsnArgAla	160
Db	634	GAANAATGGATCATCACCGATGACACGGTTTCAGTTCCAGCAAAAGAACTCGAACCGGGCC	693
QY	161	GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsn	180
Db	694	GGTTTTGGGACAGACAGATCTGCCACGTGGCATAACTTCAACGCCCCGGAAGCTAAAT	753
QY	181	MetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe	200
Db	754	ATGTCAGAGGCAGTCCCGAAGCTGAAGCGGTTATGTTTGGAGCGTTAGATTTCCTCTTC	813
QY	201	GluLysThrGlyLeuLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe	220
Db	814	GAGAAAAACCGGAATTAACCGCGCGAAGTCGGAATCTTGATAGTAACCTGCAGCTTAATC	873
QY	221	AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle	240
Db	874	AATCCAGCGCGTCTCTATTCACGATGATCGTGAACCATTACAAAGATGAGAGAAGACATC	933
QY	241	LysSerTyrAsnLeuGlyLeuMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla	260
Db	934	AAAAGTTACAACCTCGGAGGAATGGTTGCTCCGCCGGAATTAATCTCAATTCGATTCGCT	993
QY	261	AsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIle	280
Db	994	AACAATCTCTCAAAGCAAAACCCCTAATCTTACGCTGCTGTAAGACGCGGAAACATA	1053
QY	281	ThrLeuAsnTyrTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg	300
Db	1054	ACCCTAACCTGGTACTTCGGAATAGCCGGTCAATGCTCTCTGCAACTGCATCTCCGA	1113


```
/evidence-not_experimental
/product="T25K16.6"
/protein_id="AAF26474.1"
/db_xref="GI:6715647"
/translation="MDNTSGEELLAKARKPYTITKORERWTEDEHERFLLEALRLYGR
AMORIEHIGTKTAVOIRSHAKFFTKFGKAHSEWFTFOLEKEAEVKIGIPVCOALDIE
IPPRPKRKENTPYPRKGNNGTSSOVSSAKDAKLVSSASSOLNOAFDLKXPFES
ERTSTKRENDENGSGYSTYKYLPLTKVSGDIEFTSKTSTVDNAVODVPKKNKDKGN
DGTTVISMOMY PWHFHADIVNGNIACPKQHPGSMVSDQFMFPMREETHGHANLOAT
TASATTTASHQAEPACHQDODYRFLQISSTF SNLIMSTILLONPAHAAATFAASVWP
YASVNGSDSTSPSSPPSITAATAATAAATAWASHGLLPVCAPIATCVPFSTV
AVPIEMEDMTVENTQPFKQNTALQONLASKSPASSDDSDDETGVTKLNAUSKTN
DKTIEVVVTAHDSNTAQKNLVRSSCGSNTPGSDAFTDALDKMEKDKEDVKT
DENQVIELNRIKIRMDNRNNNTTDSKVESEBERIAFOALFRERLIPQSFSP
QVANEVRKSDTSMPLAPNFKSODSCAADOEGVMVGVTCKSLIKTQTFKPKYKRC
SMEVKESOVGINNOODEKVKRLRLEGEAST"
complement(join(38600..38756,38838..38989,39111..39516,
39915..40031,40377..40579))
/note="similar to Medicago truncatula Mtn2 gi|3193308;
similar to EST gb|H77065"
/codon_start=1
/evidence-not_experimental
/product="T25K16.7"
/protein_id="AAF26473.1"
/db_xref="GI:6715646"
/translation="MAGDMQGVVRVEKYSPIVMNSNVAMGVSVALVKKALDVGYNH
MVIGAYMAISAILLVPFAYVLERSLIMQFFLLGLSYTSATVSCALVSLMLPAITFAL
```

```
Alignment Scores:
Pred. No.: 5 69e-238 Length: 86436
Score: 2680.00 Matches: 520
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
```

US-09-883-797-2 (1-520) x AC007323 (1-86436)

QY	181	MetSerGluAlaAaTqAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe	200
Db	58116	ATGTCAGAGGACGCGCGGAAGCTTATGTTGGAGCCTTAGATCCCTCTTC	58057
QY	201	GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe	220
Db	58056	GAGAAACCGGAATTAAACCGCGCGGAAGTTCGAATCTTGATAGTAACTGACAGCTATTTC	57997
QY	221	AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle	240
Db	57996	AATCCGACGCGCTCTTATCAGCGATGATCGTGAACCATTAAGATGAGAGAACACATC	57937
QY	241	LysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla	260
Db	57936	AAAAATTACAACTCGGAGAAATGGGTTCCTCCGCGGATTAATCTCAATCGATCTCGCT	57877
QY	261	AsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIle	280
Db	57876	AACAATCTCTCAAGCAACCCCTAATCTTACGCTGCTCGTGGTAAGCACGGAACACATA	57817
QY	281	ThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg	300
Db	57816	ACCTTAACCTGGTACTTCGGAATGACCGGTCAATGCTCTCTGCAACTGCATCTCCGA	57757
QY	301	MetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyr	320
Db	57756	ATGGCGGAGCTCGGATTCCTCTCTACCCGCGCTCAAGCCGGAAGTCAAGGTAC	57697
QY	321	SerLeuValAsnValValArgThrHisLysGlySerAspLysAsnTyrAsnCysVal	340
Db	57696	TCGCTGGTCAACGTCGTTCAACACATAAAGGATCAGACACAAAGAACTACAATTGCTG	57637
QY	341	TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer	360
Db	57636	TACCAGAGGAGACGAGAGAGAACATCGGTGTCTCTTACCTAGAGAGCTCATGTCT	57577
QY	361	ValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeu	380
Db	57576	GTCGCGGAGAGCGCTCTGAAACAAACATCACGACTTTAGGACCGATGTTCTTCATTC	57517
QY	381	SerGluLysLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysVal	400
Db	57516	TCAGAGAGTTGATGTTCTTCAATTCCTTGGTCAAAAGGAAGATGTTCAAGTTAAAGTT	57457
QY	401	LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly	420
Db	57456	AAACCGTATATTCGGATTTCAAGCTAGCTTTCGAGCATTTCTGTATTCCACGAGGAGT	57397
QY	421	ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluPro	440
Db	57396	AGAGCGGTCTTAGACGAAGTGCAGAAGAAATCTTGATCTCAAGATTTGGCACATGAACT	57337
QY	441	SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMet	460
Db	57336	TCTAGAATGACTTTCACAGATTTGGTAAACACTTCGAGTACGCTTGGTATGAGATG	57277
QY	461	AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe	480
Db	57276	GCATTATACCGAAGCTAAGGTCGGGTAAAGCTGGTACCACCTTTGGCAGATTCGCTT	57217
QY	481	GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu	500
Db	57216	GGATCGGTTCAAGTGTAAATAGTGGCGTTTGGAAAGCGTTTACACCGGTTTCGACGGAG	57157
QY	501	GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValGln	520
Db	57156	GAGATACCGGTAATGCTTGGGTGCTTCGATTCATCAATATCCGGTTAAAGTTGTGCA	57097
RESULT	7		
LOCUS	AP004939/c		
DEFINITION	Lotus japonicus genomic DNA, chromosome 1, clone: Lj17M09, TM0105,		
	127990 bp	DNA	linear
	PLN 19-JUL-2002		

Thu Feb 20 11:03:33 2003

us-09-883-797-2.p2n.rge

complete sequence.

ACCESSION AP004939

VERSION AP004939.1 GI:21907955

KEYWORDS HTG.

SOURCE Lotus japonicus DNA, clone_lib:LjT library clone:LjT17M09.

ORGANISM Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE

1 Kaneko, T., Nakamura, Y., Asamizu, E., Kato, T., Sato, S. and Tabata, S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Sixty-six TAC clones which cover the 6.7 Mb Regions of the Genome

Unpublished

2 (bases 1 to 127990)

Direct Submission

NAKAMURA, Y.

Institute, Department of Plant Gene Research, 1532-3, Yana,

Kisarazu, Chiba 292-0812, Japan (E-mail: ynekazusa.or.jp,

URL: http://www.kazusa.or.jp, Tel: 81-438-52-3935,

Fax: 81-438-52-3934)

Location/Qualifiers

1. 127990

/organism="Lotus japonicus"

/db_xref="taxon:34305"

/chromosome="1"

/clone_lib="LjT library"

/note="TAC clone:FW0105"

40715 a 22938 c 23288 g 41049 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 3 34e-176 Length: 127990

Score: 2020.50 Matches: 390

Percent Similarity: 84.04% Conservative: 47

Best Local Similarity: 75.00% Mismatches: 80

Query Match: 75.39% Indels: 3

DB: 8 Gaps: 3

US-09-883-797-2 (1-520) x AP004939 (1-127990)

QY 1 MetaspargluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValIle 20

Db 86961 ATGGACAAAGAGATTAAACGGCTGAGATGACTTCAAGACTCCACCTCCGCGCTCATC 86902

QY 21 ArgIleArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeu 40

Db 86901 AAAATCCGGCAGCGTTCGGGATTTCTCCAGACGGTGAAGCTAAAGTACCTTAAGTTA 86842

QY 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeu 60

Db 86841 GGTTACGGCTACAGCTGTAAGCTGCCACCGTTCTCATTTTCATCTTCCCTCTC 86782

QY 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80

Db 86781 ATCCGTGTTCTCTCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 86722

QY 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100

Db 86721 TCGGACCACACGGTCCACCTCCACACCGACACG--GTCACCGGTTTCAGCGGTGCTGCTG 86665

QY 101 PheValLeuThrLeuThrValAlaAsnArgSerLysProValTyrLeuValAspPheSer 120

Db 86664 TTCCTGTTGGACTCTACTTGGCGAAGCGGTGGCGCCCGGTTTACCTTTGGGATTTTCGCG 86605

QY 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140

Db 86604 TGCTACACCGGAGAAAGCGCAAAATCTCGTGGATTCTCTCTCAAAATGACAGAG 86545

QY 141 GluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsnArgAla 160
 Db 86544 GAGACTGGAGGGTTTGAGGAGGAGACGCTCCAATTCAGCGAAGAAATTTCAATGAAGCG 86485
 QY 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsn 180
 Db 86484 GGTCTGGGGACGAGACTTATCTTCCAAAGGAATCAGTCCGCGCCACCAATCTGTGC 86425
 QY 181 MetSerCysAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe 200
 Db 86424 ATGAAGAACGCGGTTTGGAGCGGAGCGGTGATGTTCCGAGCCATGGATCTCTGTTT 86365
 QY 201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
 Db 86364 GCGAAACAGGGTTAACCCGGAAGACATTCGATCTGGTGGTGAATTTGCGATCTGTT 86305
 QY 221 AsnProThrProSerLeuAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
 Db 86304 AACCCGACGCGCTCGCTCTCCGCCATGATTGTGAACCATTAACAAGTAGGACCAACATC 86245
 QY 241 LysSerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla 260
 Db 86244 AAGAGCTACAACCTCGCGGGAATGGTTCAGCGAGGCTAATTTCCATTGATCTGGCG 86185
 QY 261 AsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValIleSerThrGluAsnIle 280
 Db 86184 AAGGACCTTTCGAGCGGGAATCCGAATTCCTACGCGGTGGTGGTGGACGAGAGATATT 86125
 QY 281 ThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg 300
 Db 86124 ACCCTCAATTGGTACTTCGGAAACGACCGCTCCATCTCTGCAACTGCATTTCCCG 86065
 QY 301 MetGlyGlyAlaAlaIleLeuLeuSerAsnArgArgGluAspArgLysLysSerLysTyr 320
 Db 86064 ATGGGTGGTGGCGGCTGCTCTCTCGAAACAATCCTCAGACAGGCGCAATCAAGTAC 86005
 QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
 Db 86004 GAGCTGGTCCACGCTGGCGGCCACCAAGGGGTCCGATCACAAGCACTACAACCTGGTG 85945
 QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
 Db 85944 TACCAATGGAGCAGAGAGAGGGGAAAGTGGGTGTTGTTGGCGAGGAGCTCATGGCG 85885
 QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeu 380
 Db 85884 GTGGCGGAGATGCTCTGAAACGAACATTACAACGCTGGGGCGCTGGTCTGCGCGTTT 85825
 QY 381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMet---PheLysLeuLys 399
 Db 85824 ATGGACGAGTTTCATGTTCTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 85765
 QY 400 ValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGly 419
 Db 85764 AGCAAGCGGTACATACCGGATTTCAAGCTACGCTTCGAGCATTTCTGATCCACCGCA 85705
 QY 420 GlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGlu 439
 Db 85704 GGAAGACGGTGTGGAGAGATGCAAGAAATCTTGAACCTCAGTGGTGGCAGATGGA 85645
 QY 440 ProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGlu 459
 Db 85644 CCGTCTCGGATGACACTGCACCGTTTCGCAACACTTCTAGTAGTCTCCCTCTGTTACGAG 85585
 QY 460 MetAlaThrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAla 479
 Db 85584 CTTCCCTACACCGAAGCAAGCGCGGTTCGCAAGGGGACCGGCTCTGCGAGATCGCA 85525
 QY 480 PheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProVal---Ser 498
 Db 85524 TTTGGTGGCTTTCAGCTGTAACGCGCGTGTGAAGCGGTGCGCGATATGATGCGCGAA 85465
 QY 499 ThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518


```

Db 85464 CTAGGGGACTGGCGGCGACACCATCGGATCGATTGATAAGTACCCGGTTAAATGTT 85405
RESULT 8
AF082033
LOCUS
DEFINITION
Hemerocallis hybrid cultivar. 1929 bp mRNA linear PLN 15-JUL-1999
(SAL5) mRNA, complete cds.
ACCESSION
AF082033
VERSION
AF082033.1
KEYWORDS
GI:3551959
SOURCE
Hemerocallis hybrid cultivar.
ORGANISM
Hemerocallis hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Hemerocallidaceae; Hemerocallis.
1 (bases 1 to 1929)
Panavas,T., Pikula,A., Reid,P.D., Rubinstein,B. and Walker,E.L.
Identification of senescence-associated genes from daylily petals
Plant Mol. Biol. 40 (2), 237-248 (1999)
99339248
PUBMED
10412903
REFERENCE
2 (bases 1 to 1929)
Panavas,T., Pikula,A., Reid,P.D., Rubinstein,B. and Walker,E.L.
Direct Submission
Submitted (04-AUG-1998) Biology, University of Massachusetts,
Morrill Science Center, Amherst, MA 01003, USA
Location/Qualifiers
1..1929
/organism="Hemerocallis hybrid cultivar"
/cultivar="Stella d'oro"
/db_xref="taxon:80862"
/tissue_type="senescing petals"
1..1929
/gene="SAL5"
5..1558
/gene="SAL5"
/function="fatty acid elongase"
/note="mRNA accumulates in senescing petals and
accumulation is induced by exogenous ABA"
/codon_start=1
/product="senescence-associated protein 15"
/protein_id="AAC34858.1"
/db_xref="GI:3551960"
/translation="MDKERLTAPMFRDSSIVIKIRKLPDFLQSVKLYVKLYGRST
TKPPTLLLPULLIAASLFRHTHTLTFTANFIDFTVAFSSSIALLLLVVYTRRP
RPVYLDFACYKPEDEHKISNEGFLMEFTSTTAFNDKSLIDFQTKIVRSGLGETYLP
PGIOARPPKLSMAEARLEATVMFGCLDALFESTGINSPRDIGILVNCSLFNPFTPL
SAMIVNHVKMRDVKVFNLGGMGCSAGLISIDLAKDMLQANPNYSALVLSFENITLNM
YFGNDRSMLLSNCIFRMGGAVALLSNKRDKAKRKYRLHHTVTRHGADDSYCNVYQ
REDEGKVCVSLAKELMAYAGALKNTITLGLVPLPLTEQGFPLATLITRKLLKLG
VRPYTPNKRFAFEHFCVHAGGRVLDVEKNLGEKTDMEASRSVLHFRFGNTSSSLW
YELATNEAKRGVKGDRVWQIGVSGFKNSAVWKAMKDVPAIDRTASGSRMCPWG
DCIDRYPVK"
BASE COUNT 533 a 414 c 478 g 504 t
ORIGIN

Alignment Scores:
Pred. No.: 8, 18e-155 Length: 1929
Score: 1764.00 Matches: 351
Percent Similarity: 79.06% Conservative: 68
Best Local Similarity: 66.23% Mismatches: 85
Query Match: 65.82% Indels: 26
DB: 8 Gaps: 9

US-09-883-797-2 (1-520) x AF082033 (1-1929)

Qy 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValIle 20
|||||
Db 5 ATGGACCGAGAACGACTCAGCGCTCAGATGGCTTCACAGAC---TCCTCCATTGTCATC 61
|||||
Qy 21 ArgIleArgArgLeuProAspLeuThrSerValLysLeuLysTyrValLysLeu 40
|||||
Db 1106 CTAGTGTGGCGGTGACGGAAACAGGGGAAATTTCTGGCAACTTTGATTACGAGAAAGTTG 1165
|||||

```

/chromosome="3"
/clone="OSJNB0096L14"
/clone_lib="ECORI"
BASE COUNT 35707 a 30896 c 29581 g 34958 t
ORIGIN

QY 396 PheLeuLeuLys---VallysProTyrIleProAspPheLysLeuAlaPheGluHisPhe 414
Db 1166 CTTAAACTGAAAGGGGTGAGCGGTACATTCCTCAAAATTTAAACCGCGATTGTGACACTTC 1225

QY 415 CysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLys 434
Db 1226 TGGCTGCAGCTGGGGCAGCAGCTGTTGGATGAGTCTGAGAAAGATCTGGGCTTGGAG 1285

QY 435 AspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSer 454
Db 1286 AAGACAGACATGGAGGCGATCGAGAAGCGTCTCCACCGGTTTGGGAACACTAGTAGCAGC 1345

QY 455 SerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArg 474
Db 1346 TCGCTGTGGTATGAGCTGGCTTACAATGAGCAAAAGGGGAGAGTCGGAAGGGGTGATCGA 1405

QY 475 LeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeu 494
Db 1406 GTTGGCAGATGGGTTGGTTCGGGTTCAAGTGTACAGTGCAGTGTGGAAGGCCATG 1465

QY 495 ArgProValSerThrGluGluMetThrGly-----AsnAlaTrp 507
Db 1466 AAAGACGTTCCGGCAATGATCGAACACCTAGTGGCTTCTCGAATGTGCAATCCGTGG 1525

QY 508 AlaGlySerIleAspGlnTyrProValLys 517
Db 1526 GGGGATTGCATTGACCGCTACCCAGTCAAG 1555

RESULT 9
AC129008 131142 bp DNA linear PLN 24-JUL-2002
LOCUS Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNB0096L14, from chromosome 3, complete sequence.
AC129008
AC129008.1 GI:21954009

HTG.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 131142)
McCombie, W.R., de la Bastide, M., Spiegel, L., Preston, R.,
Nascimento, L., Zutavern, F., Balija, V., Bell, M., Miller, B.,
Muller, S., Katzenberger, F., Sullivan, P., Yang, C., Dike, S.,
O'Shaughnessy, A., Palmer, L. and Dedhia, N.
Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNB0096L14, from chromosome 3, complete sequence
Unpublished

2 (bases 1 to 131142)
McCombie, W.R.
Direct Submission
Submitted (24-JUL-2002) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30);
an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest.

The nucleotide sequence of this clone was generated by combining
Syngenta and Cold Spring Harbor Laboratory Genome Research Center
sequencing data. OSJNB0096L14 overlaps clone OSJNB0078P24
(AC118672) from base 1 to base 9426. The overlap is from base
138843 to base 148268 on OSJNB0078P24.

Location/Qualifiers
1. 131142
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"

FEATURES
Source

Alignment Scores: 3,38e-148 Length: 131142
Pred. No.: 1720,50 Matches: 338
Score: 76,52% Conservat: 76
Percent Similarity: 62,48% Mismatches: 86
Best Local Similarity: 64,20% Indels: 41
Query Match: 8 Gaps: 8
DB:

US-09-883-797-2 (1-520) x AC129008 (1-131142)

QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSer----- 16
Db 56991 ATGGAGCGGAGCGGCTACGGCGGAGATGGCTTCGCGGACGACGCGCGGCGCGCGG 57050

QY 17 -----SerAlaValIleArgIleArgArgLeuProAspLeuThr 31
Db 57051 GGGAGTGGGCGCGGAGCATCTGATCAAGATCGGCGCGCTCCCGGACTTCGCGCGG 57110

QY 32 SerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSerCysAsnValThrThrIle 51
Db 57111 TCGGTGAACCTCAAGTACGTCAAGCTCGGATCGGCGGACGCGGCGGCTCAGCTCG 57167

QY 52 LeuPhePheLeuIleLeuProLeuThrGlyThrValLeuValGlnLeuThrGlyLeu 71
Db 57168 -----TACCTGCCCCATGCTGTGCGTGGCGTGTCTCGCCCTCCGCGCGCTAC 57212

QY 72 ThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaValGlnLeuAspThrAlaThr 91
Db 57213 TCCTTC-----GTCCGCTCGACCTCATCTAC 57239

QY 92 Arg-----LeuThrCysLeuValPheLeuSer-----PheValLeuThr 104
Db 57240 CGGTCCATCGACCTGCTCACCTGCTGCGCTGGCGCGCGCGCTGTCTGTCTCACC 57299

QY 105 LeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysPro 124
Db 57300 GTCTACTTCAAGCGCGCGCGCTGTACCTCGTGTGCTGTCTGTCTGTCTGTCTGT 57359

QY 125 GluAspGluArgLysLysSerValAspSerPheLeuThrMetThrGluGluAsnGlySer 144
Db 57360 GACGACGACGACAAAGATCTCCAAGGAAGGCTTCTTCGAGATGACCGGAGGACCGGCTGC 57419

QY 145 PheThrAspAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAsp 164
Db 57420 TTCAATGACGCGCGCTCGACTTCCAGACCAAGATCACCACATCGCTCCGCTCGCGGAC 57479

QY 165 GluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAla 184
Db 57480 GAGAGTACCTCCCTCCCGCGCTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57539

QY 185 ArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGly 204
Db 57540 AGGATGGAGCGCGCGCGCTCATGTTTCGGGTGCTCGCTCGCTCGCTCGCTCGCTCG 57599

QY 205 IleLysPro---AlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThr 223
Db 57600 ATCAACCCGAAACGCGACGCTGGGCACTCTCATCTGACGCTCTTCAACCCGCGCG 57659

QY 224 ProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspLysSerTyr 243
Db 57660 CGCTGCTGCTGCTGATGATCATCAACCACTACGATGCGGCGGCGGCGGCGGCGGCTTC 57719

QY 244 AsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeu 263
Db 57720 AACCTCGGCGGATGGGGTGACGCGCGGCGCTCATCGCCATCGACCTCGCGGACGACATG 57779

QY 264 LeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsn 283

Thu Feb 20 11:03:33 2003

```
Db 61415 GAGGCCCGCAAGGAGGCGCGCATGTTCTCGGCGCATTTACACAGCTTCTTTGAGAG 61474
Qy 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61475 ACGGTGTGAACCCCAAGGACATGTTGGTGTCTGCTCAATGCGAGCTTTCAACCCG 61534
Qy 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61535 ACGCGTGTCTGCGCCATGTTGTGAACCACTACAAAGTGAGGGGGAATGTCATCAGC 61594
Qy 243 TyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsp 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61595 TACAACCTCGGGGATGGGTGCACTGCGGCTTGTCTGCGATCTGCGCAAGGAC 61654
Qy 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61655 TTGCTGCAGGTGACCAAACTCGTACGCGCTGGTGTGACGATGGAGAACATCACGCTC 61714
Qy 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61715 AATTGTFACCTTTGGCAACACCGGTGATGCTGTCGAAATTCCTTCCGATGGGC 61774
Qy 303 GlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysSerLysTyrSerLeu 322
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61775 GCGCGCGCCATCTGCTGTCGAACAGCGGTGCGACCGCGCGGAGGTCCAAGTATCAGCTT 61834
Qy 323 ValAsnValValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGln 342
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61835 GTGCACACCGTGGCGACGACAGGCGCCAAACGACAAAGTCTTTGGCTGTCCACCCAG 61894
Qy 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61895 GAGGAGACGAGATCGCGACAGATCGCGGTGCTCTCAAGGACCTGATGGCGGTGCC 61954
Qy 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGlu 382
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61955 GGAGACCGCTGAGACGACATCACCCCTCGGCGCGCTGCTCTCCGTTGTCCGAG 62014
Qy 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLeuLysValLysPro 402
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62015 CAGCTGTCTTCAATGGCCACATGTTGCCAAGAGGTCCTCAAGATGAAGATCAAGCCA 62074
Qy 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAla 422
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62075 TACATTCGCGATTCAAGCTGCATTTGAGCATTTCTGCATCATCGCGGTGGCGTGCC 62134
Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62135 GTGCTGGATGAGCTGGAGAAGAACTGGAGTTGACTGACTGGACATGAGGCAATCAGG 62194
Qy 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62195 ATGACACTGTACCGTTTGGCAACACATCGACAGCTCACTCTGATGATGAGTGGCGTAC 62254
Qy 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62255 ACCGAGCGAAGGAGGATCAGGAAGCGGACAGGATCTGGCAGATTCATTTGGATCT 62314
Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62315 GGTTCAGTGAACAGCGCATCTCGAAGCGGCTGCAACACATGAATCCAGCGAAG--- 62371
Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62372 GAGAAGACCCCTGGATGATGAGATTGACAACTTCCCGTTGAAGTT 62419
RESULT 11
AC098832 139028 bp DNA linear HTG 03-NOV-2001
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) chromosome 5 clone
QJ1268B08, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.
ACCESSION
AC098832
VERSION
AC098832.1 GI:16603960
```

```
HTG: HTGS, PHASE2.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 119028)
Chow,T.-Y., Hsing,Y.-I.C., Liu,S.-M., Chen,C.-S., Shaw,J.-F.,
Chen,H.-H., Chao,Y.-T. and Wu,H.-P.
Oryza sativa BAC OJ1268B08 genomic sequence
Unpublished
2 (bases 1 to 119028)
Chow,T.-Y. and Hsing,Y.-I.C.
Direct Submission
Submitted (03-NOV-2001) Institute of Botany, Academia Sinica, 128,
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and ASPC-Taiwan sequencing data.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 47212: contig of 47212 bp in length
* 47213 47222: gap of unknown length
* 47223 50050: contig of 2828 bp in length
* 50051 50060: gap of unknown length
* 63358 63358: contig of 13298 bp in length
* 63359 63368: gap of unknown length
* 63369 111339: contig of 47971 bp in length
* 111340 111349: gap of unknown length
* 111350 119028: contig of 7679 bp in length.
* Location/Qualifiers
  1..119028
    /organism="Oryza sativa (japonica cultivar-group)"
    /cultivar="Nipponbare"
    /db_xref="taxon:39947"
    /chromosome="5"
    /clone="OJ1268B08"
BASE COUNT 32106 a 27418 c 26704 g 32758 t 42 others
ORIGIN
Alignment Scores:
Pred. No.: 5,77e-144 Length: 119028
Score: 1674.50 Matches: 317
Percent Similarity: 77.42% Conservative: 67
Best Local Similarity: 63.91% Mismatches: 105
Query Match: 62.48% Indels: 7
DB: 2 Gaps: 3
US-09-883-797-2 (1-520) x AC098832 (1-119028)
Qy 25 ArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsn 44
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77746 CCGCTGCGGACTTCAAGCAATCGTGAAGTCAAGTACGTCGAGTGGGTACAC 77802
Qy 45 SerCysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrVal 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77803 -----TACCTCATCACACCGCGCGTACCTCTCGCCCGCTCCGGGCTCGTG 77856
Qy 65 LeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAla 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77857 GCGGGCGACCTCTCCACCTTACGCTGGCGGACCTCGCGGCAAAAC----- 77910
Qy 85 ValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThr 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77911 CTCAGTACAACTCGTCTCCGCTGCTCTGCTCCACGCTGCTGCTCTCCAC 77970
Qy 105 LeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysPro 124
```


DB:	8	Gaps:	4
US-09-883-797-2 (1-520) x ZMA292770 (1-2018)			
Qy	23	ArgArgLeuPro-AspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLe 42	
Db	198	CGAGGGCGTTCCGGGAGTCCAGCAGTCAAGTGGCGCTCAAGATGTGAAGCTGGGTA 257	
Qy	42	uHisAsnSerCysAsnValThrThrLeuLeuPhePheLeuLeuLeuLeuProLeuThrG1 62	
Db	258	CCAC-----TACCTCATATCCACCGGATGACCTGCTGCTGCGCGCTGATGGC 308	
Qy	62	yThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuThrPheSerAs 82	
Db	309	GCTCGTCCGCGTCCAGCTCCACCGCTCCCGCGCATGACCTCGCGCGACCTGTGG----- 363	
Qy	82	nGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheVa 102	
Db	364	-GAGCAGCTCCCGTTCAACCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422	
Qy	102	lLeuThrLeuThrValAlaAsnArgSerLysProValThrLeuValAspPheSerCysTy 122	
Db	423	CTCCACCGTTTACTCTCCACCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482	
Qy	122	rLysProGluAspGluArgLysLeuValAspSerPheLeuThrMetThrGluGluAs 142	
Db	483	CAAGCGGAGTCGGAGCGCAAGTGCACGCGCGAGACCTTCATGCACTGCTCCCAAGCTCAC 542	
Qy	142	nGlySerPheThrAspAspThrValGlnPheGlnArgLysSerAsnArgAlaGlyLe 162	
Db	543	CGATCTCTCCAGCGAGAGAACCTCGAGTTCACGCGCAAGATCTCGAGCGCTCCGGCCT 602	
Qy	162	uGlyAspGluThrTyrLeuProArgGlyLeuThrSerThrProProLysLeuAsnMetSe 182	
Db	603	CGCGAGGACACGTACCTTCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662	
Qy	182	rGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLy 202	
Db	663	CGAGGCGCGTAAGAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722	
Qy	202	sThrGlyLeuLysProAlaGluValGlyLeuLeuLeuValAsnCysSerLeuPheAsnPr 222	
Db	723	GACCGGTGTGAGGCGCAAGGACATGTGTCTAGTGTCTCACTGACGCGCTGTTCACGCC 782	
Qy	222	oThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSe 242	
Db	783	GACCGCGTGTGTCACCATGGTGGTGAACCATTCACAGCTGAGGGGGAATATTGTGAG 842	
Qy	242	rTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuLeuSerIleAspLeuAlaAsnAs 262	
Db	843	CTACAACCTCGCGGGATGGCTGCAGCGCGGGGCTC-----ATCGACCTCGCCAAAGA 896	
Qy	262	nLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLe 282	
Db	897	TCTGCTGAGGTGACCCCACTTACGCGCTGCTGATCATCATGAGGAGAACATCATCAT 956	
Qy	282	uAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetG1 302	
Db	957	GARTTGGTACCTTGGGAACAACCGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016	
Qy	302	yGlyAlaAlaLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLe 322	
Db	1017	TGGCGCGCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076	
Qy	322	uValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrG1 342	
Db	1077	GGTGCACAGGTGGCGACGACAGAGGCGCGCAACAGCTGCTTCCGCTGCTGCTGCTGCTGCT 1136	
Qy	342	nLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAl 362	
Db	1137	GGAGCAAGATGAGATTGGCAAGATTGGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1196	
Qy	362	aGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerG1 382	
Db	1197	CGGAGCGCAGCTTAAGACCAACATCACCGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1256	
Qy	382	uGlnLeuMetPheLeuLeuSerLeuValLysArgLysMetPheLysLeuLysValLysPr 402	
Db	1257	GCAACTTCTCTCATGGCACATTTGATGCGCAAGAGTGTCTCAAGATGAAAATCAAGCC 1316	
Qy	402	oTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAl 422	
Db	1317	ATACATCCCTGACCTCAAGCTGGCTTTCGAGCACTTCTGATCCACGACGCGCGCGCGC 1376	
Qy	422	aValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerAr 442	
Db	1377	TGTGCTGATGAGTGGAGAGAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1436	
Qy	442	gMetThrLeuHisArgPheGlyAsnThrSerSerSerSerSerSerSerSerSerSerSer 462	
Db	1437	GATGACCTGATGAGTGGCAACACATCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1496	
Qy	462	rThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySe 482	
Db	1497	CACCTGAGCAAGAGGTAGGATCAGGAGCGCGACAGGATCTGCGCAGATCGCATTTGGTTC 1556	
Qy	482	rGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMe 502	
Db	1557	TGATTAAGTCAACAGCGCGCTGCTGGAAGCAGCTCCCGAGCGGTGAACCGCGCCCAAG-- 1614	
Qy	502	tThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518	
Db	1615	-GAGAAGAGCCCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662	
RESULT 13			
AC003105		95167 bp DNA linear	PLN 27-FEB-2002
LOCUS	Arabidopsis thaliana chromosome 2 clone F18A8 map B68, complete		
DEFINITION	sequence.		
ACCESSION	AC003105		
VERSION	AC003105.3	GI:20197019	
KEYWORDS	HTG.		
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 95167)		
AUTHORS	Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Kaul, S., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 95167)		
AUTHORS	Lin, X.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA		
REFERENCE	3 (bases 1 to 95167)		
AUTHORS	Town, C.D. and Kaul, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, cdtown@igr.org		
COMMENT	On Apr 18, 2002 this sequence version replaced gi:6598390.		
FEATURES	Location/Qualifiers		
source	1..95167		
	/organism="Arabidopsis thaliana"		
	/cultivar="Columbia"		
	/db_xref="taxon:3702"		
	/chromosome="2"		
	/map="B68"		
	/clone="F18A8"		
	1..178		
misc_feature			
	/note="overlap with BAC clone T9J22 (AC002505:115674..115851)."		
	86..1745		
gene			
	/gene="At2g26640"		

mRNA

/note="F18A8.1"
<86..1745

CDS

/gene="At2g26640"
86..1615
/gene="At2g26640"
/codon_start=1
/product="putative beta-ketoacyl-CoA synthase"
/protein_id="AAB95298.1"
/db_xref="GI:2760830"

/translation="MDVEQKPLIESSDRNLPDFKSKVKLVKLYGHLITHGMFLF
LSPVLVIAQISTFVSVDLRLSLEHLQYNIISVVVCSMLLVFLFIYFMTFRPRPVYL
VNSCFPDESRSKTKKIFMDRSKLGTSTFTEENLEFQRKILQCSGLGESTVLPFAVLN
VPNCPKKEAKETVYFAGIDELLAKTNPKDGIILVQCSLNFPTPSLSAMVNV
HYKLRNLSYNLGCMGCSAGLISDIKALLHLLSPNTYAMVISWENITLWYFENDR
SKLVNCLFRMGGAAILLSNKRWRDRRSKYELVDTVRHKGADCKFCGICITQEDSDS
KIGVTLSEKELMAGADAKNTITLPLVLTTSQLLFATLVGRKKLPMKIKPYIPD
FKIAFEHCTHAGGRAVLDELKLNKLITHEHMEPSRMTLYRFGNTSSSLWYELAYE
AKGRIKGDRIQWJAFSGFKNSVWRAVRKSNPKKEKNPMDIEIHFPPVEVPKST
I"

gene

complement(1934..6493)
/gene="At2g26650"

/note="F18A8.2: identical to GB:U06745; supported by cDNA:
gi.2569932.emb_x62907.1.ATAKT1"

mRNA

complement(join(<1934..2789,2883..2958,3053..3247,
3350..3535,3659..3691,3774..3872,3962..4207,4289..4606,
4715..4772,4842..5198,6264..6493))
/gene="At2g26650"

CDS

complement(join(1957..2789,2883..2958,3053..3247,
3350..3535,3659..3691,3774..3872,3962..4207,4289..4606,
4715..4772,4842..5198,6264..6436))
/gene="At2g26650"

/codon_start=1

/product="K+ transporter, AKT1"

/protein_id="AAB95299.1"

/db_xref="GI:2760831"

/translation="MRGKSLNSQIETLPWDRKFLSKYKELKKLKLMEPRSVENRP
LRRFVSPDHYKRIWEAFVLVLTAVWSPFEFLKRPPLSLTIDNIVNAFFAI
DIIMTFVGLDKSTYLVDDRQIAFKYLRSCAKLVCLDTIPSEAMRISSSQSGIF
NMLRWRRLRGALFARLEKDRNFYFWRCALVCVTLFVHCAACFYLIARNS
PAKTIGANVANFLESWMRYVTSWYSITTLTVGYGDLHPVTKEMTDFIDYMLF
NLGLTAYLIGNTNLVHCTSRNRPDTIOAASFNRHNLPRLODMQLAHLCIKY
RPTSEGLQOQETLDLPAKIRSSISHFELYSMDKYLFRGVSNLDLILFVLSKKA
FPKEDVILQNEAPTDYILVNGTADLVVDYGTESIYREVKAGDIIIGEVLCYRQ
LTVTRKCOLLRNRTFLNIQANVGDTIIMNNLOHLKEMDPVNTVLLIE
NMLARKGDLPLNCFALREDDDLHLQLKGLDPNEDNNGRTPLHIAASKGLTNC
VILLLEYHADPNCRDAEGSVPLWEAMVEGHEKVKVLLHSGTIDAGDVHFACTAAE
QGNLKLKEIVLHGGDVTFRATGTSALHTACEENIEMVKYLLEOGADVKNQDMHW
TPRDIAEQOQHEDIKALFREKLHRRVHTETSSVPIKGTIRFLGRPTSEPNIRAS
REVSPRIETRRARRKTNFNDSLFGILANQSVKNGLATVDEGRGNPVRVTISCAEK
DDIAGKLVLLPGSPKLELLESLGFGIVATKYVKNKDNNAEIDDDVDVIRGDGHLIFAT
S"

repeat_region

complement(8035..8068)
/rpt_family="(TA)n"

gene

8924..10695
/gene="At2g26660"

/note="F18A8.3"

mRNA

join(<8924..9214,9644..9770,10250..>10695)
/gene="At2g26660"

CDS

join(8924..9214,9644..9770,10250..10695)
/gene="At2g26660"

/codon_start=1

/product="unknown protein"

/protein_id="AAB95300.1"

/db_xref="GI:2760832"

/translation="MRGKSLNSQIETLPWDRKFLSKYKELKKLKLMEPRSVENRP
NKRSRSDVDTPTVGMTKEELDFISLLEDELEKENSFFVEQEEYIIRLKLKDO
VAKAKNEEMINTKKEIVDFHGMVILMNY SALNYGLAKILKYDKRTAKILRLE
IQVLPQPFPTDLLNTFVKECEAMLDRLPFSNKSRLNDEGEPTSGMVTGTDSE
LLRVPKELSETEYELMSYKSTVSALKVLKEIRSGSSVSVFSLPPASGLEDDSWK
KKYGVLEQVAK"

repeat_region

complement(11326..11345)
/rpt_family="(A)n"

gene

11711..113532

/gene="At2g26670"
/note="F18A8.4: identical to GB:AF132475; annotation
updated per Seth J Davis at University of Wisconsin
Madison; supported by full length cDNA: Ceres: 33692"
join(11711..12231,12887..13110,13186..13532)
/gene="At2g26670"
join(11808..12231,12887..13110,13186..13386)
/gene="At2g26670"
/codon_start=1
/product="heme oxygenase 1 (HO1)"
/protein_id="AAB95301.2"
/db_xref="GI:4883666"
/translation="MAYLAPISSLSIFKNPQSRFOFSSSSPNPLFLRPRIQLISM
MKNPSLVVVAATAAEKOKKRYPGESGRFVAMRLHTDKOAKEGEKETSMT
ERVAKWEPTVEGLRELVDKLVYDTLELIQDSNEPTYAEFNKTLGERAEKLSIDL
ENFKEGEYETPEPTAPCKTYSQYLKELAEKDPQAFICHFYNIYFAHSGAGGRMIGRKA
ERILDKLELFYAKDWELSQLQNNREKLNKAAEETREKHNKCLEETKFSKYSGEI
LRILLS"
complement(13832..15377)
/gene="At2g26680"
/note="F18A8.5: supported by full length cDNA:
Ceres:41755"
complement(join(<13832..14354,14681..>15377))
/gene="At2g26680"
complement(join(13995..14354,14681..15280))
/gene="At2g26680"
/codon_start=1
/product="expressed protein"
/protein_id="AAB95303.1"
/db_xref="GI:2760835"
/translation="MASAWKDKNOKLSPKTLISLLVLSIFLSSLFFFSNLSQV
SNPINSPPYIPDFPCFKQSKPIANVENLKYFVYSLADLGNLPEKPHNTV
RLKKGPKRPDISATIQEVLDSMRASGKNGIVVDYGANVMASFAAAMVGMKFLVE
PVFENLRICDGIWENRVASLVTFEAAASDRGTDLTEHLKVLGRLDNSAVSEVGARLA
PKSKEIAVQVKS IPLDKLIPPSQPVLLIKIDVOGHEYHVLKAGKALLSGKPAEAPYL
IYEDERLLLTASNSSSKERDFLKSVGKSCSHQGTDAHCTKE"
15154..15222
/rpt_family="(GAGAA)n"
complement(15547..15620)
/rpt_family="AT-rich"
complement(15772..15810)
/rpt_family="AT-rich"
complement(15830..15883)
/rpt_family="AT-rich"
complement(16293..16320)
/rpt_family="AT-rich"
complement(16416..16507)
/rpt_family="AT-rich"
complement(17203..21441)
/gene="At2g26690"
/note="F18A8.6"
complement(join(<17203..17859,17945..18291,18370..18675,
18765..19000,19277..19494,20718..20820,21412..>21441))
/gene="At2g26690"
complement(join(17339..17859,17945..18291,18370..18675,
18765..19000,19277..19494,20718..20820,21412..21441))
/gene="At2g26690"
/codon_start=1
/product="putative nitrate transporter"
/protein_id="AAB95302.1"
/db_xref="GI:2760834"
/translation="MVRFSIVSGEESKSWTVADAVDYKGRPADKSKTGGWITAAAIL
GIEVRLSTMGIAVLNLTVMETMHLPSSTSANIVTDFMGTSFLLCULLGFLADSLF
GRKPTIGISTIOALGALAVATKLPRLPPTCHHGCAIPATAFQMTILYLSYLI
ALGTGGLKSSISGFGQDFDDKPKRAHMAFFNFFVIFSMGTLAAAFRRKMLPQ
VGRSWAGICTVSMIAIIVFLCQTKRYRKQSGSPVQIFQVIAAARFRKMLPQ
SIVLYEDNPEGRIETDQFLHDKAIVAEQDFEOTLDGVAIPNPKWLSVTVKVEE
VMMVRLLPWTATIIIFWTTTAQMITESQOASTMRNIGSKFIPAGSLTVFVVAAIL
ITLAVDRAIMPFWKWKPKGPFSSLQRIAGIIVLSTAGMAAALVEOKRLSVAKSS
OKTLPISVLLVPQFELVAGAEFIYTGOLDFFITQSPKGMKMTGLTLLTSLGIF
VSSFLSVIKRVSTSTDVGLADININHRUDYFYLLVILUSLGNFVVIICALMFKP
TKGKDSVEKENGKGFVEDC"
20028..20062

repeat_region

repeat_region /rpt_family="AT_rich" complement(20153..20180)
repeat_region /rpt_family="AT_rich" complement(20399..20422)
repeat_region /rpt_family="AT_rich" complement(20666..20691)
repeat_region /rpt_family="(TA)n" complement(21447..21474)
repeat_region /rpt_family="(TA)n" complement(24028..24078)
repeat_region /rpt_family="(CAAAA)n" complement(24617..24636)
repeat_region /rpt_family="(A)n" complement(25109..25133)

Alignment Scores:
Pred. No.: 8,67e-141 Length: 95167
Score: 1639.00 Matches: 304
Percent Similarity: 78.38% Conservative: 84
Best Local Similarity: 61.41% Mismatches: 101
Query Match: 61.16% Indels: 6
DB: Gaps: 3

US-09-883-797-2 (1-520) x AC003105 (1-95167)

QY 24 ArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHis 43
DB 128 CGTAATCTACCTGATTTCAAAAAATCAGTGAAGCTTAATAATGTGAAGCTTGGTTACCAT 187
QY 44 AsnSerCysAsnValThrIleLeuPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 63
DB 188 -----TACCTATACCTCATCGAATGTACCTTTTCCCTCCCTCCCTTACCTGTA 238
QY 64 ValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuLeuThrPheSerAsnGln 83
DB 239 ATCGCTGCACAGATTTCAACTTCTCTGTCACCGATCTTCGTAGCTCTGGAGCAT--- 295
QY 84 AlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeu 103
DB 296 ---CTTCAGTACAACTTATCTCAGTGGTGTGTTGTTCTTCTGCTGCTGCTTCTTAAG 352
QY 104 ThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLys 123
DB 353 ACTATTTACTTCATCAGTCCGACCGCTCTGCTACTTCTGTTGTTGTTGTTGTTGTTGTTAA 412
QY 124 ProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGly 143
DB 413 CCGATGAGTCACGAAATGCACTAAAGATCTTTATGGATGCTTCTAACTCACTGGC 472
QY 144 SerPheThrAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGly 163
DB 473 TCTTTCACAGAGGAGAACTTCAGTTCACGCTAAGATCTACACGTTCCGGGCTCGG 532
QY 164 AspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGlu 193
DB 533 GAATCGACTTACTTACCCGAGCTGTACTTAATGTTTCCGCTAACCCGTTATGAAGAA 592
QY 184 AlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThr 203
DB 593 GCTCGAAAGAGCGGAGACTGTATGTTGGAGCTTATGATGAGCTTCTTTCGAGACG 652
QY 204 GlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThr 223
DB 653 AATGCAACCCGAGGATATGGATCTTGTATGTTTAACTGTAGTTGTTTAAACCCGACA 712
QY 224 ProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyr 243
DB 713 CACTTCGTTATCTGCTATGTTGTTTAACTACTATAGCTCCGCGGAATATCTAGTTAC 772
QY 244 AsnLeuGlyLysMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeu 263
DB 773 AACTTGGGGAATGGTTCAGTGTGTTGATTTCTATGTTCTGCTAATCACTCT 832

QY 264 LeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsn 283
DB 833 CTTCACTCTATCCCAACACTTATCAATGGTATAGTATGATGAGAACAATACGTTGAAC 892
QY 284 TrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGly 303
DB 893 TGGTATTTCCGGATGACCGGTTCGAAGCTTGTCTTAATTTGTTTGAATGGGAGGT 952
QY 304 AlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuVal 323
DB 953 GCAGCGATTCTCTTTTCGAACAAAAGATGGGACAGGATGGAAGATCGAATAATGAGCTGTT 1012
QY 324 AsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLys 343
DB 1013 GATACGGTTAGGACTCACAAAGGAGCTGATGATGATGATGATGATGATGATGATGATGAT 1072
QY 344 GluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGly 363
DB 1073 GAGGATTCGCAAGTAAAGATTGGTGTACCTTCTCGAAGAACTTATGGCTGTTCGGGT 1132
QY 364 AspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGluGln 383
DB 1133 GATGCTCTAAAGACAAATATACGACGTTAGGACCACTGCTTTTACCGCATCTGAACAG 1192
QY 384 LeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyr 403
DB 1193 CTTCTCTCTTTCGCAACGTTAGTGGGAAGAAACTCTTCAAGATGAAGATCAACCTTAC 1252
QY 404 IleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaVal 423
DB 1253 ATCCAGACTTCAAACTAGCTTGGTGTGACATTTCTGCATCCACGAGGAGGAGAGCTGTT 1312
QY 424 LeuAspGluValGlnLysAsnLeuAspLeuLysAspThrPheLysMetGluProSerArgMet 443
DB 1313 CTTGATGAATTGAGAAGAACTTGAACTCACAGAGTGGCATATGGAGCCCTCGAGGATG 1372
QY 444 ThrLeuHisArgPheGlyAsnThrSerSerSerLeuTyrTyrGluMetAlaTyrThr 463
DB 1373 ACATCTACCGTCTTGGTAAACGCTCCAGTCTCTCTTCTGTTGATGATGATGATGATGAT 1432
QY 464 GluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGly 483
DB 1433 GAGCCCAAGAGGAGGATCAAGAAAGTGTATAGAAATTTGGCAGATAGCTTTTGGTTCGGG 1492
QY 484 PheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThr 503
DB 1493 TTCAAGTGCACACAGCTCGGTTTGGAGAGCGGTAAAGTTCGTAACCCCTAAGAAA---GAG 1549
QY 504 GlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
DB 1550 AAGAACCCATGGATGGATGAATTCATGAGTCCAGTCCAGTTCAGATC 1594
RESULT 14
AF424620 1803 bp mRNA linear PLN 08-OCT-2001
LOCUS Arabidopsis thaliana AT5g43760/MQD19_11 mRNA, complete cds.
DEFINITION AF424620.1 GI:15983490
ACCESSION AF424620.1
VERSION FLI_CDNA.
KEYWORDS Arabidopsis thaliana.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis;
1 (bases 1 to 1803)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Bah, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, X.,
Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A.,
Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE Arabidopsis cDNA clones

JOURNAL
REFERENCE
AUTHORS

Shinn, P., Chen, H., Cheuk, R., Kim, C. J., Koesema, E., Meyers, M. C., Banh, J., Bowser, L., Carnipino, P., Dale, J. M., Goldsmith, A. D., Hayashizaki, Y., Ishida, J., Jiang, P. X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J. M., Lin, J., Liu, S. X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C. S., Palm, C. M., Pham, P. K., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C. C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J. R.,

Direct Submission
Submitted (26-SEP-2001) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES
SOURCE

```

Location/Qualifiers
1. .1803
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="5"
/clone="RAPL09-07-G05(R14419)"
/note="ecotype: Columbia"
1. .130
131. .1720
/note="beta-ketoacyl-CoA synthase"
/codon_start=1
/product="AT5G43760/MQBP19_11"
/protein_id="AAAL11613.1"
/db_xref="GI:15983491"

```

3'UTR	BASE COUNT	ORIGIN
WIDEIDDFPVQVPRITPSS ^a	496 a	476 c
1721..1803	330 g	501 t

Alignment Scores:		
Pred. No.:	5.59e-142	1803
Score:	1626.00	Matches: 308
Percent Similarity:	76.51%	Conservative: 73
Best Local Similarity:	61.85%	Mismatches: 107
Query Match:	60.67%	Indels: 10
DB:	8	Gaps: 4

US-09-883-797-2 (1-520) x AF424620 (1-1803)

QY 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45


```
QY 86 GlnLeuaspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
Db 393 CATTTCTCTCCGCCACACTCGCCACCGCACTC-----TTAATCTCTCTCCACCGCT 446
QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
Db 447 TACTTCACCCCGTCCCGCGGTCTCTCTCCGACTTCTCTCGACTTCTCGTTACAAACGAGAC 506
QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
Db 507 CTTTCACTGATCTGCACCTCGTGAACATTCATGGACAGATCTCAACGCTAGGCATCTTC 566
QY 146 ThrAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAspGlu 165
Db 567 ACAGAAGACAACTTAGCTTTTCCACAAAGATCTCGAAAGATCCGGTCTAGGTCAGAAA 626
QY 166 ThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAlaArg 185
Db 627 ACTTACTTCCCTGAAGCTCTTCTTCGTGTTCTCTCTAATCTCTGTATGGAAGACGGAGA 686
QY 186 AlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyIle 205
Db 687 AAGAGGCAGAAACAGATATCTCGGAGCTATTGACGGGTTCTTTGAGAAGACCGGTGTG 746
QY 206 LysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThrProSer 225
Db 747 AAACCTAAGATATGGAAATCCTTGGTGAAATGTAGCTGTGTTTAAATCCACACCGTCA 806
QY 226 LeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeu 245
Db 807 CTTTCTGCTATGATGTGAATAAGCTTAAGCTTAGAGCAACATTTTGAGCTATAATCTT 866
QY 246 GlyClyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLys 265
Db 867 GGTGGAATGGATGAGTGTGCTGGGCTTATCTCCATTGATCTCGCTAAACAGATGCTTCAG 926
QY 266 AlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnThrPyr 285
Db 927 GTGCAACCAACTCATACGCACTAGTGGTGAGCAGACAGAAACATAAACCTAACTGGTAC 986
QY 286 PheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAla 305
Db 987 TTAGGCAACGACCGATCAATGCTTCTATCTAACTGATCTTCGCTATGGCGGAGCCGCG 1046
QY 306 IleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnVal 325
Db 1047 GTACTTCTCTGAACCGCTCTCTGTGATCGCAGCGCTTCAAAATATCAGCTCATCCATACC 1106
QY 326 ValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLysGluAsp 345
Db 1107 GTCCGTACCCACAAAGAGCTGATGACAAACCATTTGGCTGTGTTTACCACGAGAGAC 1166
QY 346 -----GluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerVal 361
Db 1167 AACAAACGAGAAGAACCGCGCAAAATCGGAGTGTCCCTCTCTAAAAACCTAATGGCGATA 1226
QY 362 AlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSer 381
Db 1227 GCTGGAGAAAGCTCTCAAGACAAACATCACAACCTCTCGACCACTAGTTCTACCAATGTCC 1286
QY 382 GluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu--LysVal 400
Db 1287 GAACAACTTCTCTTTTCGGGACCTCTTGTGGCCCGAAAGTCTTCAAAAGTCAAGAAATA 1346
QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
Db 1347 AAGCCTTACATTCTGTATTTCAAGCTAGCTTTCGAGCATTTCTGTATCCACGCGGAGGT 1406
QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLysAspTrpHisMetGluPro 440
Db 1407 AGAGCCGTGCTCGACGAGATTGAGAAGAACTTGGATTTATCCGAATGGCACATGGAGCCA 1466
```

```
QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMet 460
Db 1467 TCGAGGATGACGTTTGAACCGGTTTGGTAACACTTCGAGTAGCTCACTTTGGTATGAGCTT 1526
QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
Db 1527 GCGTATAGTGAAGCTAAAGGAAGATTAAAGAGAGAGATAGGACTTGGCAGATTGCTTTT 1586
QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
Db 1587 GGATCGGGTTTAAAGTCTAATAGTGCAGTTTGAAAGCTTTGAGAACGATTGATCCAATG 1646
QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1647 GACGAGAAGACTAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1700
```

Search completed: February 19, 2003, 10:27:15
Job time : 3735 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 08:32:32 ; Search time 315 Seconds
(without alignments)
3717.585 Million cell updates/sec

Title: US-09-883-797-2

Perfect score: 2680

Sequence: 1 MDRRLTAEMAFRDSSAVI.....EMTGNWAGSIDQYPVKVQ 520

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapext 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool/US09883797/runat_14022003_102500_19495/app_query.fasta_1.711
-DB=N_Geneseq.101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATR=Dlosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09883797.cgn_1.1.396/runat_14022003_102500_19495 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEXTIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2680	100.0	1560	20	AA2323217	A. thaliana EL1 DN
2	1647	61.5	1747	21	AAC37360	Arabidopsis thalia
3	1639	61.2	1720	21	AAC47402	Arabidopsis thalia
4	1626	60.7	1821	21	AAC50606	Arabidopsis thalia
5	1619	60.4	1824	21	AAC39957	Arabidopsis thalia
6	1601	59.7	1732	16	AAQ90219	Condensing enzyme
7	1598	59.6	1807	20	AAZ28316	Fatty acyl-CoA elo
8	1595.5	59.5	2143	22	AAH50968	Ketoacyl ACP synth
9	1588.5	59.3	1587	21	AAC42814	Arabidopsis thalia
10	1563	58.3	1548	20	AAZ23223	Arabidopsis thalia
11	1531.5	57.1	1611	20	AAZ23221	A. thaliana EL7 DN
12	1531.5	57.1	1853	21	AAC50224	A. thaliana EL5 DN
13	1519.5	56.7	1783	16	AAT04124	Arabidopsis thalia
14	1519.5	56.7	1783	16	AAQ90208	Jojoba wax-synthas
15	1513.5	56.5	1819	21	AAC39559	Jojoba fatty acyl-
16	1510.5	56.4	1855	21	AAC37776	Arabidopsis thalia
17	1497	55.9	1733	14	AAQ42839	Arabidopsis thalia
18	1497	55.9	1733	16	AAT04123	Jojoba fatty acyl
19	1497	55.9	1733	16	AAQ90207	Jojoba wax-synthas
20	1442.5	53.8	1704	16	AAQ90217	Jojoba fatty acyl-
21	1441	53.8	1650	20	AAZ32320	Condensing enzyme
22	1438.5	53.7	1502	20	AAZ32322	A. thaliana EL4 DN
23	1438.5	53.7	1840	21	AAC4659	A. thaliana EL6 DN
24	1438.5	53.7	1857	21	AAC45219	Arabidopsis thalia
25	1438.5	53.7	3722	20	AAV84180	Arabidopsis thalia
26	1438	53.7	1949	21	AAC33574	Arabidopsis thalia
27	1438	53.7	2008	21	AAC49056	Arabidopsis thalia
28	1432	53.4	1810	16	AAQ90210	Arabidopsis thalia
29	1426.5	53.2	1523	21	AAC39308	Brassica condensin
30	1419.5	53.0	1464	21	AAC42778	Arabidopsis thalia
31	1419.5	53.0	2509	22	AAZ62693	Arabidopsis thalia
32	1401	52.3	1482	21	AAZ51486	Maize ZmKCS1 prote
33	1401	52.3	1954	21	AAZ50706	Maize ZmKCS1 prote
34	1392	51.9	1584	21	AAZ35525	Fatty acid elongas
35	1323.5	49.4	1512	20	AAZ32319	A. thaliana EL3 DN
36	1317.5	49.2	1521	24	AAD28518	A. thaliana FAEL-B
37	1314.5	49.0	1521	24	AAD28511	B. napus elongase
38	1313.5	49.0	1521	24	AAD28520	A. thaliana FAEL-B
39	1310.5	48.9	1521	24	AAD28507	A. thaliana FAEL-B
40	1308.5	48.8	1521	24	AAD28519	A. thaliana FAEL-B
41	1307.5	48.8	1521	24	AAD28510	A. thaliana FAEL-B
42	1307.5	48.8	1521	24	AAD28515	Brassica napus elo
43	1306.5	48.8	1524	24	AAD28516	Brassica napus fat
44	1306.5	48.8	1785	22	AAF61744	B. napus KCS cDNA
45	1306.5	48.8	1785	22	AAF61746	B. napus KCS cDNA

ALIGNMENTS

RESULT 1
AA2323217
ID AA2323217 standard; DNA; 1560 BP.
XX
AC AA2323217;
XX
DT 11-JUN-1999 (first entry)
XX
DE A. thaliana EL1 DNA.
XX
KW EL1; very long chain fatty acid; VLCFA; beta-keto acyl synthase;
KW plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;
KW pharmaceutical; edible oil; ss.
XX
OS Arabidopsis thaliana.
XX
FN WO9854954-A1.
XX

Thu Feb 20 11:03:34 2003

us-09-883-797-2.p2n.rng

PD 10-DEC-1998.
 XX
 PF 01-JUN-1998; 98WO-US11384.
 XX
 PR 03-JUN-1997; 97US-0868373.
 XX
 XX (CRGI) CARGILL INC.
 PA (JAWO) JAWORSKI J G.
 PA (POST) POST-BEITTENMILLER MA.
 PA (TODD) TODD J.
 XX
 XX Jaworski JG, Post-Beittenmiller MA, Todd J;
 XX WPI; 1999-070227/06.
 DR P-PSDB; AAW93427.
 XX
 XX New isolated beta-keto acyl synthase polynucleotides - used
 PT particularly for the production of transgenic plants having altered
 PT levels of very long chain fatty acids in tissues
 XX
 XX Claim 9; Fig 3; 76pp; English.
 XX
 CC This invention describes the isolation of beta-keto acyl synthase
 CC proteins from Arabidopsis thaliana. The products of the invention
 CC can be used for producing vegetable oils having elevated levels of
 CC very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels
 CC and as a feedstock for plastics, pharmaceuticals and cosmetics. The
 CC products can also be used for producing oils having reduced levels of
 CC VLCFAs for use as edible oils. This sequence encodes ELL.
 XX
 XX Sequence 1560 BP; 420 A; 355 C; 378 G; 407 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 3,19e-273 Length: 1560
 Score: 2680.00 Matches: 520
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-883-797-2 (1-520) x AAX23217 (1-1560)

QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerAlaValile 20
 Db 1 ATGGATCGAGAGAGATTAAACGGCGAGATGCGGTTTCGAGATTATCATCGCGGTATA 60
 QY 21 ArgileArgArgLeuProAspLeuThrSerVallysLeuLysTyrVallysLeu 40
 Db 61 AGAATTCGAAGAGCGTTTTCGGGATTTATTAACGTCCTTAAGCTCAAAATACGTGAAGCTT 120
 QY 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeu 60
 Db 121 GGACTTCACAACTCTTGCACGTGACACCATCTCTCTCTTCTTAATATTCTTCTCTTTA 180
 QY 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80
 Db 181 ACCGGAACCGTGGTTCAGCTAACCGGTCTAACGTTTCGATACGTTCTCTGAGCTTTGG 240
 QY 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100
 Db 241 TCTAACACGGCGGTTCACACTCGACACGGCGAGACACTTACCTGGTTTCTCTCTCC 300
 QY 101 PheValLeuThrLeuTyrValAlaAsnArgSerIysProValTyrLeuValAspPheSer 120
 Db 301 TTCGTTTGGACCTCTACGTGGCTAACCGGTCTAACCGGTCTTACCTAGTGGATTCTCC 360
 QY 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140
 Db 361 TGCACAAACCGGAGACGCGTAAATATATCAGTAGATTCGTCTTGGACGATGACTGAG 420
 QY 141 GluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsnArgAla 160
 Db 421 GAAATGGATCATTCACCGATGACACGGTTTCAGTCCACAAAGAAATCTCGAACCGGGCC 480

QY 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsn 180
 Db 481 GGTTCGGAGACGAGACGATATCTGCCACGTTGGCATACTTCAACGCCCCCGAAGCTAAAT 540
 QY 181 MetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe 200
 Db 541 ATGTCAGAGCAGCGTCCGGAAGCTGAAGCGCTTATGTTGGAGCTTATAGATTCCTCTTC 600
 QY 201 GluLysThrGlyLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
 Db 601 GAGAAAACCGGAATTAAACCGCGCGAATCTGATAGTAACTGAGCTTATTC 560
 QY 221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
 Db 661 AATCCGACGCGCTCTCTATCAGCGATGATCTGTAACCATACAGATGAGAGAAGACATC 720
 QY 241 LysSerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla 260
 Db 721 AAAAGTTACAACCTCGGAGGAATGGTTGCTCCGCGGATTAATCTCAATCGATCTCGCT 780
 QY 261 AsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValValSerThrGluAsnIle 280
 Db 781 AACAACTCTCTCAAGCAACCCCTAATCTTACGCTGCTGCTGTAAGCACGGAACACATA 840
 QY 281 ThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg 300
 Db 841 ACCCTAACTGCTACTTCGGAATGACCGGTCAATCTCTCTGCAACTGCATCTTCCGA 900
 QY 301 MetGlyGlyAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyr 320
 Db 901 ATGGCGGAGCTGGGATTCCTCTCTAACCCCGCTCAACGCGGAAGTCAAGATGAC 960
 QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
 Db 961 TCGTGGTCAAGCTGCTCGAACACATAAAGGATCAGACGACAAAGAACTACAATTCGCTG 1020
 QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
 Db 1021 TACCAGAAAGAGACGAGAGAGAACAAATCCGGTGCTCTTTAGCTAGAGAGCTCATGCT 1080
 QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeu 380
 Db 1081 GTCGCGGAGACGCTCTGAAACAAACATCACGACTTTAGGACCGATGGTTCTTCCATG 1140
 QY 381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
 Db 1141 TCAGAGCAGTTGATGTTCTTGGTCAAAAGGAAGATGTTCAAGTTAAAGTT 1200
 QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
 Db 1201 AAACCGTATATCCGGATTTCAAGCTAGCTTTTCGAGCATTTCTGTATTCACGAGAGGT 1260
 QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTTPHisMetGluPro 440
 Db 1261 AGACGCGTCTAGACGAAGTGCAGAAATCTTGTATCTCAAGAAATGGCACATGGAACCT 1320
 QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrTyrGluMet 460
 Db 1321 TCTAGAAATGACTTTGCACAGATTTGGTAAACATTCGAGTACGCTCGCTTGTATGAGATG 1380
 QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
 Db 1381 GCTTATACCGAAGCTAAGGTCGGGTAAAGCTGGTACCACATTTGGCAGATTCGGTTT 1440
 QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
 Db 1441 GGATCGGGTTCAAGTGTATAGTGCCTTTTGGAAAGCGTTTACGACCGGTTTCGACGGAG 1500
 QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValValGln 520
 Db 1501 GAGATGACCGGTAATGCTTGGGCTTTCGATTTGATCAATATCCGCTTAAAGTTGTGCAA 1560

RESULT 2
AAC37360
ID AAC37360 standard; DNA; 1747 BP.
XX AC AAC37360;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17094.
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 28-MAR-1999; 99US-0126264.
PR 01-APR-1999; 99US-0126785.
PR 06-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130449.
PR 28-APR-1999; 99US-0130510.
PR 30-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 17-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142920.
PR 13-JUL-1999; 99US-0142977.
PR 14-JUL-1999; 99US-0143542.
PR 15-JUL-1999; 99US-0143624.
PR 16-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 27-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.

[illegible]

```
Db 884 GCAGCGATTCTTCTTCGACAAAGACATGGACAGAGAGATCGAAATATGAGCTTGT 943
QY 324 AsnValValAlaThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLys 343
Db 944 GATACGGTTAGGACTCACAAAGGAGCTGATAGTGTTCGGTTCATACCAAGAA 1003
QY 344 GluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGly 363
Db 1004 GAGGATCCGCAAGTAAGATTGGTTCCTGCGAAAGAACTTATGCTGTTCGGGT 1063
QY 364 AspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGluGln 383
Db 1064 GATGCTCTAAAGACAAATATTACGACGTTAGCACCATCTGTTTACCGACATCTGAACAG 1123
QY 384 LeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyr 403
Db 1124 CTTCTGTCTTGTGACAGCTTAGTGGGAAGAAACTCTTCAAGATGAAGATCAAGCCTTAC 1183
QY 404 IleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaVal 423
Db 1184 ATCCAGACTTCAAACTAGCCTTTGAGCATTTCTGCATCCAGCAGGAGGAGAGCTGTT 1243
QY 424 LeuAspGluValGlnLysAsnLeuLysLeuLysAspTrpHisMetGluProSerArgMet 443
Db 1244 CTTGATGAATGGAGAGAACTTGAACCTCACAGATGGCATATGGAGCCCTCGAGGATG 1303
QY 444 ThrLeuHisArgPheGlyAsnThrSerSerSerLeuTyrTrpTyrGluMetAlaTyrThr 463
Db 1304 ACATCTACCGTTTGTGTAAACACGTCACGTTCTTCTTGTGTGTATGAATATGATATAGT 1363
QY 464 GluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGly 483
Db 1364 GAGCCAAAGAGAGGATCAAGAAAGGTAGATAATTTGGCAGATAGCTTTTGTTCGGGG 1423
QY 484 PheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluLysMetThr 503
Db 1424 TTCAAGTGCACAGCTCGGTTGGAGAGCGGTAAAGCTCGGTAAACCTTAAGAAA---GAG 1480
QY 504 GlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1481 AGAACCCATGGATGGATGAATATTCATGAGTTCCTCCAGTTGAAGTC 1525

RESULT 4
AAC50606
ID AAC50606 standard; DNA; 1821 bp.
XX AC AAC50606;
XX AC AAC50606;
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65464.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
PD 06-SEP-2000.
XX PF
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
```


Db 740 AAACCTAAAGATATCGAATCCTTGTTGGTGAATGTAGCTGTGTTAATCAACACCGTCA 799
QY 226 LeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeu 245
Db 800 CTTTCGTGCTATGATCTGAATAGTATAAGCTTAGAGGCAACATTTTGAGCTATAATCTT 859
QY 246 GlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLeuLys 265
Db 860 GGTGAATGGGATGTAGTCTGGCCTTATCTCCATTGATCTCGCTAAACAGATGCTTCAG 919
QY 266 AlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyr 285
Db 920 GTGCAACCAAACTCATACCGCTAGTGTGAGCAGACAGATAACCTTAAACTGGTAC 979
QY 286 PheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAla 305
Db 980 TTAGCAACGACCGATCAATGCTTCTATCTAACTGATCTCCGTATGGCGGAGCGCG 1039
QY 306 IleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuValAsnVal 325
Db 1040 GTACTTCTCGAACCGCTCTCTGATCGACGCCGTTCAAATATATCAGCTCATCAATAC 1099
QY 326 ValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLysGluAsp 345
Db 1100 GTCCGTACCCAAAGGAGCTGATGACCAACGATTTGGCTGTGTTTACCAACGAGAAGAC 1159
QY 346 -----GluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerVal 361
Db 1160 AACACGCGAGAGAACCGCAAAATCGAGTGTCCCTCTCTAATAAACCTAATGGGATA 1219
QY 362 AlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyPrometValLeuProLeuSer 381
Db 1220 GCTGGAGAAGCTCTCAAGACAAATCATCAACTCTCGACCACTAGTCTTACCAATGCC 1279
QY 382 GluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu---LysVal 400
Db 1280 GAACAACCTTCTTTTCGCGACTCTGTGGCCCGAAAGTCTTCAAAAGTCAAGAAAAATA 1339
QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
Db 1340 AAGCCTTACATTCCTGATTTCAAGTAGCTTCGAGCATTTCTGTATCCACGCGGAGGT 1399
QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluPro 440
Db 1400 AGAGCCGTGCTCGACGAGATGAGAACAACTTGGATTTATCCGAATGCCATGGAGCCA 1459
QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMet 460
Db 1460 TCGAGGATGACGTTGAACCGTTTGGTAAACATTCGAGTAGCTCACCTTGGTATGAGCTT 1519
QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
Db 1520 GCGTATAGTAGAAGCTAAAGGAAGGATTAAGAGAGAGATAGGACTTGGCAGATGCTTTT 1579
QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
Db 1580 GGATCGGGTTTAAAGTGTATAGTGCAGTTTGGAAAGCTTTGAGAACCATGATCCCAATG 1639
QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1640 GACGAGAGACTAATCCATGGATGTGATGATGATGATGATGATGATGATGATGATGAT 1693
RESULT 5
AAC39957
ID AAC39957 standard; DNA; 1824 BP.
XX AC AAC39957;
XX AC AAC39957;
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26523.
XX

Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.
Arabidopsis thaliana.

PN EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 24-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139763.
PR 22-JUN-1999; 99US-0139817.
PR 23-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.

[illegible]

Thu Feb 20 11:03:34 2003

Best Local Similarity:	61.35%	Mismatches:	105
Query Match:	59.74%	Indels:	12
DB:	16	Gaps:	5
US-09-883-797-2 (1-520) x AA090219 (1-1732)			
QY	23	ATGATGAGLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeu 42	
DB	97	CAAAACAATCTCCCAATTTCTCTTATCTGTTCCGGCTCAATATGTAATAAATCTGGGTAC 156	
QY	43	HisAsnSerCysAsnValThrThrLeuPhePheLeuLeuLeuLeuLeuProLeuThrGly 62	
DB	157	CAT-----TACCTAATCTCCAAACGGCTCTACATCTCCCTCCCTCCTCCTCGGC 207	
QY	63	ThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuThrSerAsn 82	
DB	208	GGCACAATCGTAACACTCTCTCTCCACACTCAACGAACCTCTCTCTCTCTCAACACC 267	
QY	83	GlnAlaValGlnLeuAspThrAlaThrArgLeuThr---CysLeuValPheLeuSerPhe 101	
DB	268	CTCGGTTTTCATTTCTCTCTCCGCACACTCGCTACCGGACTCTTAATCTCTCTCTCC--- 324	
QY	102	ValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCys 121	
DB	325	-----ACCGCTACTTCAACACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 378	
QY	122	TyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGlu 141	
DB	379	TACAACTGACCTTCTCTTAATATGCACTCGTGAACATTCATGGACCGATCTCAACGT 438	
QY	142	AsnGlySerPheThrAspThrValGlnPheGlnArgIleSerAsnArgAlaGly 161	
DB	439	GTAGTATCTTCACAGAAAGAACCTCGCTCTTTCACAAAGAGATCTCTCGAAGATCCGGT 498	
QY	162	LeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMet 181	
DB	499	CTTGGGAGAAACTTACTTCCCTGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 558	
QY	182	SerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGlu 201	
DB	559	GAAGAAGCGAGAAAGAGAGAGACTGTTATGTTCCGGAGCTATAGACTCTGTTCTTGAG 618	
QY	202	LysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsn 221	
DB	619	AAACCGGTGTGAACCTTAAGATATCGAATCTTGTGTAATGTTGTTGTTGTTAAT 678	
QY	222	ProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLys 241	
DB	679	CGAGCGCGTCACTTCCGCCATGATGTTGAATAGATATAAGCTTAGAGAGAAACATTTTG 738	
QY	242	SerTyrAsnLeuGlyClyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsn 261	
DB	739	AGCTATAATCTCGGTGGAATGGTGTAGTGTGGACTATCTCCATTTGATCTCGCTAAA 798	
QY	262	AsnLeuLeuLysAlaAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThr 281	
DB	799	CAGCTTCTCAGTCCCAACCAACTCATACCGCTAGTGTGTGACGACAGAGAACATAACC 858	
QY	282	LeuAsnTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMet 301	
DB	859	TTAAACTGTGTACTTAGGCAACGACCGCATCAATGCTTCTCTACTACTCTCTCTCTCT 918	
QY	302	GlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysSerLysTyrSer 321	
DB	919	GGAGAGCGCGCTACTTCTCAACCGTTCCTCCGATCGCACCCGCTTCAAAAATATCAG 978	
QY	322	LeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyr 341	
DB	979	CTCATCCACCGCTCGCTACCAACAAAGAGCCCAACACGACATTTGGCTGCTTAC 1038	
QY	342	GlnLysGluAsp-----GluArgGlyThrIleGlyValSerLeuAlaArgGlu 357	
DB	1039	CAACGAGAGAACAAACAGAGAGAAACCCGCAAAATCGGAGTCTCACTCTCTCAAAAAC 1098	

QY	358	LeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetVal 377	
DB	1099	CTAATGGCAATAGCCGGAGAGCTCTCAAGACAAACATAACCACTCGGACCACTAGTC 1158	
QY	378	LeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLys 397	
DB	1159	TTACCAATGTCCGAACAGATTCTGTTTTCACCACTCGTGGCTCGAAATAATCTTCAAA 1218	
QY	398	Leu---LysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIle 416	
DB	1219	GTCAAGAAATAAAGCCCTTACATACCCGATTTCAAGCTAGCTTCGAGCATTTCTGCATC 1278	
QY	417	HisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTyr 436	
DB	1279	CATCGGGAGGTAGAGCAGTCTGTATGATAGATAGAGAATAATTTGATTTATCAGAGTGG 1338	
QY	437	HisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeu 456	
DB	1339	CATATGGACCATCGAGGATGACTTTAAACCGGTTTGGTANTACTTCGAGTCACTT 1398	
QY	457	TyrTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTyr 476	
DB	1399	TGGTATGAACCTTCGCTAGTAGTAAGCTAAAGGAGGAGATTAGAGAGAGATAGGACTTGC 1458	
QY	477	GlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTyrLysAlaLeuArgPro 496	
DB	1459	CAAAATTCGCTTTCGATCGGATTTAAGTGAATAGTCGGTTTGGAAAGCTTTCGAGAAC 1518	
QY	497	ValSerThrGluGluMetThrGlyAsnAlaTyrAlaGlySerIleAspGlnTyrProVal 516	
DB	1519	ATTGATCCCTATTGATGAGAAGAAATCCATCCGATGATGATGATGATGATGATGATGAT 1578	
QY	517	LysVal 518	
DB	1579	TCGTGT 1584	
RESULT 7			
ID	AAZ28316 standard; cDNA; 1807 BP.		
XX	AAZ28316;		
XX	20-DEC-1999 (first entry)		
DE	Fatty acyl-CoA elongase cDNA.		
XX	Fatty acyl-CoA elongase; double bond; plant membrane; neutral lipid;		
KW	seed tissue; palmitoyl-CoA; oleoyl-CoA; biopolymer; biosynthetic pathway;		
KW	delta-5 acyl-CoA desaturase; lubricant; grease; plastic; ink; cosmetic;		
KW	surfactant; biodegrade; long shelf life; ss.		
OS	Limnanthes douglasii.		
XX	Key	Location/Qualifiers	
XX	CDS	82..1099	
XX		/*tag= a	
XX		/product=	
XX		/note= "Fatty acyl-CoA elongase"	
XX		/transl_except= (Pos: 301..303, aa: xaa)	
XX		/transl_except= (Pos: 310..312, aa: xaa)	
XX		/transl_except= (Pos: 421..423, aa: xaa)	
XX		/note= "Xaa = Unknown"	
XX	W09949050-A2.		
XX	30-SEP-1999.		
XX	12-MAR-1999; 99WO-US05471.		
XX	20-MAR-1998; 98US-0078736.		
XX	(DUPO) DU PONT DE NEMOURS & CO E I.		

XX

PI Cahoon EB, Hitz WD, Kinney AJ, Vollmer SJ;

XX WPI; 1999-591101/50.

DR P-PSDB; AAY39362.

XX

PT Nucleic acid fragments useful in the production of industrial agents

PT for eg. lubricants or cosmetics -

XX

PS Claim 7; Page 49; 54pp; English.

XX

This is the nucleotide sequence of the entire Limnanthes fatty acyl-CoA elongase. This enzyme prefers palmitoyl-CoA (16:0-CoA) as its substrate instead of oleoyl-CoA (18:1-CoA) the usual substrate for the known plant fatty acid elongase. Fatty acids are used in plant membranes and in neutral lipids that are formed for the storage of energy in developing seed tissue. This nucleotide sequence can be linked to regulatory sequences and used to transform host cells. This invention also consists of the Limnanthes douglasii delta-5 acyl-CoA desaturase cDNA (AAZ28315). The delta-5 desaturase introduces a double bond at the delta 5 position of a C20 fatty acid. Delta-5 desaturase is an enzyme which is able to further desaturate mono-unsaturated fatty acids to make poly-unsaturated fatty acids. The nucleic acid sequences of the delta-5 desaturase and fatty acid biosynthetic pathways, allowing changes to be made in the fatty acid composition of plants and or oils and to introduce new pathways in to oil seeds in order to produce new biopolymers from acyl-CoA. The oils and fatty acids produced by the genetically engineered plants have potential for use as industrial agents including lubricants, greases, plastics, inks, cosmetics and surfactants. Polyestolides derived from the 20:1 delta-5 fatty acids of Limnanthes biodegrade slower than those derived from soybean oils or oleic oils, and thus will produce industrial products with a longer shelf life.

XX

SQ Sequence 1807 BP: 496 A; 359 C; 412 G; 534 T; 6 other;

Alignment Scores:

Pred. No.:	111e-158	Length:	1807
Score:	1598.00	Matches:	296
Percent Similarity:	76.25%	Conservative:	86
Best Local Similarity:	59.08%	Mismatches:	113
Query Match:	59.63%	Indels:	6
DB:	20	Gaps:	3

US-09-883-797-2 (1-520) x AAZ28316 (1-1807)

QY	19	ValIleArgIleArgArgLeuProAspLeuThrSerValLysLeuLysTyrVal	38
DB	112	ATCGCAACCGGTGAAACACACACTACCTGATTTAAACATATCAATAAATTAACACAGTG	171
QY	39	LysLeuGlyLeuHisAsnSerCysAsnValThrThrIleLeuPheLeuIleLeu	58
DB	172	AAACTCGGTACCAT-----TACCTGATCACCACCATGGAATGTACCTGTCTCCCT	222
QY	59	ProLeuThrGlyThrValValGlnLeuThrGlyLeuThrPheAspThrPheSerGlu	78
DB	223	CCTCGCGACTAGTCTCTCGTCAAACTCAACTTTGTCCTCAAGATTTCAACGAC	282
QY	79	LeuTrpSerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPhe	98
DB	283	ATCTCG-----GACAGCTTCAGTNNAAATCTCATNTCTGCTGTTTCATCAACACTT	336
QY	99	LeuSerPheValLeuThrLeuTyrValAlaAsnArgSerLysProValLysLeuValAsp	118
DB	337	CTGTGCTCTTACTTATCTTACTTCATGACTCGTCCGCGCGGCTTTATTTGATGGAT	396
QY	119	PheSerCysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMet	138
DB	397	TTCCGCTGCTATAAACCCGACCAACTCGAAATCTACTAGAACAACTTTTATGAAGTGT	456
QY	139	ThrGluGluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsn	158
DB	457	GGTGAGAGTTTGGGCTCTTTACGGAGGATTAATTCGATTTTCAGAGGAATTAGTCGCA	516

QY	159	ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLys	178
DB	517	CGATCTGGACTTGGTGATCTACGTATTTACCTGAAGCTATCGGTATCCCGGTCAT	576
QY	179	LeuAsnMetSerGluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSer	198
DB	577	CCGTGATGAAAGCTGCGAGAGAGAGCTGAGTTCGTGATGTTGGTGCGATTGATCAA	636
QY	199	LeuPheGluLysThrGlyIleLysProAlaGluValGlyIleLeuLeuValAsnCysSer	218
DB	637	CTTTTGGAGAGACAAAGGTGAATCCGAAGGATATAGGATCTTGGTTTAAATTCGACG	696
QY	219	LeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGlu	238
DB	697	CTGTTTATGTCGACTCCCTCCCTCGTCGATGTTTAAACCACTATAAATCCCGTGG	756
QY	239	AspIleLysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuLeuSerIleAsp	258
DB	757	AACATTATAACTACATCTAGCGGAATGGTTGCAGTCTGGTTTAAATTTCCGTCGAC	816
QY	259	LeuAlaAsnAsnLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGlu	278
DB	817	TTAGCTAAAGACTTCTCGAGACAAATCCAAACACTTACGCTTTAGTTATGACACTGAA	876
QY	279	AsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIle	298
DB	877	AATATCACACTAACTGGTACATGGCAATGACCGGTCCAAACTCGTCCCAATTTGCTT	936
QY	299	PheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSer	318
DB	937	TTCCGATGGGAGAGCTGCGTCTTGTATCAACAAACCTCTGTGTAAGAAAGATCG	996
QY	319	LysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsn	338
DB	997	AAGTATCAGTTGGTTACTCCGTCGGAAGCACAAAGGTGCTGACGATAATTTGTCGCT	1056
QY	339	CysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeu	358
DB	1057	TGCATATTCGAAGAAGAACTCCACGCGCAAAATCGTGTAAACCTCTCCAAATCTA	1116
QY	359	MetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeu	378
DB	1117	ATGGCGGTGCGAGGGAGCGCTTAAGACTTAACATCAACGCTGCTGCTGCTGCTGCT	1176
QY	379	ProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu	398
DB	1177	CCAAATGTCGAACAACCTTTTGTGTCGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCT	1236
QY	399	LysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAla	418
DB	1237	AAATTAAGCCCTACATCCGACTTAAACTAGCTTTTATGATCATTTCTGATTCATGCG	1296
QY	419	GlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTyrHisMet	438
DB	1297	GGTGTGCGAGCTGTTTGGACGAGCTTGAGAGAAATTTGCAGTTTCAACCTGCACTA	1356
QY	439	GluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerLeuTrpTyr	458
DB	1357	GAGCGCTCGAATGACGTTTATCGGTTTGGTAAATACGTCGAGTAGTACTTTGTGTAC	1416
QY	459	GluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIle	478
DB	1417	GAGCTGCGGTATTCGGAAGCAACGAGGAGGATTAGAAAGGAGAAAGAGTTTGGCAGAT	1476
QY	479	AlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSer	498
DB	1477	GGGTTCGTTTGGTTTAAATGTAATAGTGTCTGCGAAAGCCTTAAAGAGCGTGTAT	1536
QY	499	ThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal	518
DB	1537	CCAAAGAAA---GAGACAACTCCATGGATGGATGATGATCCACCGATTTCCGCTGCTGT	1593

US-09-883-797-2 (1-520) x AAH50968 (1-2143)

UIS-09-883-797-2 (1-520) x AAH50968 (1-2143)

```
QY 367 LysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPhe 386
Db 1334 AAGCCACACATCACCGCTAGCCCGCTGCTCTCTCTCCGAACAGCTGCTCTT 1393
QY 387 LeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAsp 406
Db 1394 TTCAGCACCGCTGCTCGTCCGAAAGCTTCAACATGAAGTCAAGCTTATATCTCGAT 1453
QY 407 PheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGlu 426
Db 1454 TTCAGCTGGCTTCGACCATCTCTCATCCAGCGCGGAGGCGGTGATCGACGAG 1513
QY 427 ValGlnLysAsnLeuLeuLysAspTrpHisMetGluProSerArgMetThrLeuHis 446
Db 1514 CTTGAGAAGAACTGCACTACTCCCGGACACTGTGAGCGCTCAGCAATGACCTCCAC 1573
QY 447 ArgPheGlyAsnThrSerSerSerSerLeuTyrTrpGluMetAlaTyrThrGluAlaLys 466
Db 1574 AGATTGGTAATACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1633
QY 467 GlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCys 486
Db 1634 GGGCGCATGCGCGGAGCAACCGAGTGTGGCAAAATGCTTTGGAGCGGGTTTAAGTGC 1693
QY 487 AsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThrGlyAsnAla 506
Db 1694 AATAGCGCTGTCTGCGAGCATTCGCAACATCAAGCGCTCGGAGAA-----TCGCCG 1747
QY 507 TrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1748 TGGGCTCATTTATCGATGAGTACCTCAACATGTG 1783
RESULT 9
AAC42814
ID AAC42814 standard; DNA; 1587 BP.
XX AC AAC42814;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36950.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0129845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 28-APR-1999; 99US-0130891.
XX PR 30-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.
XX PR 04-MAY-1999; 99US-0132407.
XX PR 05-MAY-1999; 99US-0132484.
XX PR 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0136029.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139763.
PR 22-JUN-1999; 99US-0139817.
PR 23-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 28-JUN-1999; 99US-0140695.
PR 29-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142920.
PR 13-JUL-1999; 99US-0142977.
PR 14-JUL-1999; 99US-0143542.
PR 15-JUL-1999; 99US-0143624.
PR 16-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
```

[illegible]

QY 260 AlaAsnLeuLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsn 279
 Db 751 GCTAAACAGCTTCTCAGGTTCACCAAAATTCATATGACACTAGTACGACAGAAC 810
 QY 280 IleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnIlePhe 299
 Db 811 ATAACCCTAAACTGGTATTAGGCAACGACCGATCAATGCTCTCAAACTGCATCTC 870
 QY 300 ArgMetGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysSerLys 319
 Db 871 CGAATGGGTGGCGCCCGCTCTCTCTAACCCTCTCCGACGCTCGCGCTCCAAA 930
 QY 320 TyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCys 339
 Db 931 TACCACATCATCCACACCGCTCGTACACAAAGGATCTGACGACAAACGCCCTTAAC 990
 QY 340 ValTyrGlnLysGlu-----AspGluArgGlyThrIleGlyValSerLeuAlaArgGlu 357
 Db 991 GTTTACCAACCGGAAGCAACAGCAGCAACAAACAAATCGTCTCACTTTCCAAAAC 1050
 QY 358 LeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetVal 377
 Db 1051 CTAATGGCTATAGCTGGAGAGCTCTCAAGACGAACATAACCACTCTGGACCGCTAG 1110
 QY 378 LeuProLeuSerGluGlnLeuMetPheLeuLeuSerLeuValLysArgLysMetPheLys 397
 Db 1111 CTACCAATGTCTGAACACTTCTCTTTTCGCAACACTAGTGGCGCGAAAGCTTTAAT 1170
 QY 398 Leu---LysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIle 416
 Db 1171 GTGAAGAAATAAAACCTTATATCCCTGATTTCAGCTAGCTTTTCGACACTTCTGCATC 1230
 QY 417 HisAlaGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLysAspTrp 436
 Db 1231 CACCGGGAGGAGAGCAGCTCGATGAGATTGAGAAGATTTCGATTATCTGAGTGG 1290
 QY 437 HisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerLeu 456
 Db 1291 CATATGGAACCTTCGAGAGTACCTTTCAACCGGTTTGAATACTTCGAGTAGCTCGCT 1350
 QY 457 TrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrp 476
 Db 1351 TGGTATGAGCTTCGTATAGTAGGCTAAAGGAGGATTAGAGAGGATAGGACTTGG 1410
 QY 477 GlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArg--- 495
 Db 1411 CAGATTGCTTTTGGATCCCGGTTTAAAGTGTAAATAGTGCAGTTCGAGAGCTTTGAGA 1470
 QY 496 -----ProValSerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGln 513
 Db 1471 ATCGATCCGTCCAAGGAGAGAGAGAGAGACTAATCCTTGGATTGATGAGATTTCATG 1530
 QY 514 TyrProValLysVal 518
 Db 1531 TTTCCGTCGCGGTT 1545

RESULT 10
 AAX23223

ID AAX23223 standard; DNA; 1548 BP.

XX AC AAX23223;

XX DT 11-JUN-1999 (first entry)

XX DE A. thaliana EL7 DNA.

XX KW EL7; very long chain fatty acid; VLCFA; beta-keto acyl synthase;

XX KW plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;

XX KW pharmaceutical; edible oil; ss.

XX OS Arabidopsis thaliana.

XX XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

PA

PA

PA

PI

DR

DR

XX

XX

PT

PT

PT

XX

XX

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-883-797-2 (1-520) x AAX23223 (1-1548)

QY 14 AspSerSerSerAlaVal---IleArgIleArgArgLeuProAspLeuLeuThrSer 32

Db 46 GATGTTCTCTGTTGGAGTTCAGATCCGACAAACACGGATGCTACCGGATTTCTCCAGAGC 105

QY 33 ValLysLeuLysTyrValLysLeuGlyLeuHisAsnSerCysAsnValThrIleLeu 52

Db 106 GTGAATCTCAAGTATGTGAATTAGTTACCAT-----TACTTAATCTCAAAATCTC 156

QY 53 PhePheLeuIleLeuProLeuThrGlyThrValLeuValGlnLeuThrGlyLeuThr 72

Db 157 TTGACTCTCTGTTTATTCCTCTCGCGTGTGTTATCTCCGTCGAGACCTTCAGATGAAC 216

QY 73 PheAspThrPheSerGluLeuTrpSerAsnGlnAlaValGlnLeuAspThrAlaThrArg 92

Db 217 CCAGATGATCTCAAAACAGCTCTGGATCCAT-----CTACAATCAATCTGGTTAGTATC 270

QY 93 LeuThrCysLeuValPheLeuSerPheValLeuThrLeuThrValAlaAsnArgSerLys 112

Db 271 ATCATCTGTTCCAGCGATTCTAGTCTTCGGGTTAAGGTTTATGTTATGACCCGACCTAGA 330

QY 113 ProValTyrLeuValAspPheSerCysTyrLysProGluAspGluArgLysIleSerVal 132

Db 331 CCGCTTTACTTGTGTTGATTCTCTGTTATCTCCACCTGATCATCTCAAGCTCTCTTAC 390

QY 133 AspSerPheLeuThrMetThrGluGlnAsnGlySerPheThrAspAspThrValGlnPhe 152

Db 391 GCTCGGTTCAAGGAACATTTAGACTACCCGAGATTTCGATGACTCTCTCGAGTTT 450

QY 153 GlnGlnArgIleSerAsnArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIle 172

WO9854954-A1.

10-DEC-1998.

01-JUN-1998; 98WO-US11384.

03-JUN-1997; 97US-0868373.

(CRGI) CARGILL INC.

(JAWO/) JAWORSKI J G.

(POST/) POST-BEITENMILLER MA.

(TODD/) TODD J.

Jaworski JG, Post-Beittemiller MA, Todd J;

WPI; 1999-070227/06.

P-PSDB; AAW93433.

New isolated beta-keto acyl synthase polynucleotides - used

particularly for the production of transgenic plants having altered

levels of very long chain fatty acids in tissues

Claim 9; Fig 15; 76pp; English.

This invention describes the isolation of beta-keto acyl synthase

proteins from Arabidopsis thaliana. The products of the invention

can be used for producing vegetable oils having elevated levels of

very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels

and as a feedstock for plastics, pharmaceuticals and cosmetics. The

products can also be used for producing oils having reduced levels of

VLCFAs for use as edible oils. This sequence encodes EL7.

Sequence 1548 BP; 401 A; 303 C; 371 G; 473 T; 0 other;

Length: 1548

Matches: 293

Conservative: 92

Mismatches: 111

Indels: 8

Gaps: 4

Thu Feb 20 11:03:34 2003

us-09-883-797-2.p2n.rng

```

Db 451 CAACGCAAGATCTTCTGAGGCTTCTGTTAGGGAGAACACTTATGTCCTCCAGCTATG 510
Qy 173 ThrSerThrProProLysLeuAsnMetSerGluAlaArgAlaGluAlaValMet 192
Db 511 CATTATGTTCCACCGAGATTTCAATGGCTGCTGCTAGAGAAGAGCTGAACAGTCTATG 570
Qy 193 PheGlyAlaLeuAspSerLeuPheGluLysThrGlyLeuLysProAlaGluValGlyLe 212
Db 571 TTTGGTGTCTTAGATAACCTTTTCGCTAACACTAATGTGAACCAAGGATATTGGAATC 630
Qy 213 LeuIleValAsnCysSerLeuPheAsnProThrProSerLeuSerAlaMetIleValAsn 232
Db 631 CTGTGTGTAATGTAGTCTCTTAATCCAACTCTCTGTTATCTGCAATGATTGTGAAC 690
Qy 233 HisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGlyGlyMetGlyCysSerAla 252
Db 691 AAGTATAAGCTTAGAGGTAACATTAGAGGCTTACAACTCTGCGGTATGGGTGCGCGG 750
Qy 253 GlyLeuIleSerIleAspLeuAlaAsnLeuLysAlaAsnProAsnSerTyrAla 272
Db 751 GGAGTTATCGCTGGGATCTTGCTAAAGACATGTTGTTGTTACATAGGACACTTATCGG 810
Qy 273 ValValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMet 292
Db 811 GTTGTCTCTTCTACTGAGAACATTACTCAGAAATGGTATTTGGTTAAACAAGAAATCGATG 870
Qy 293 LeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgArg 312
Db 871 TTGATACCGAAGCTGCTGTTTTCGAGTGTGCTGGCTGCTGCTGCTATCGAACAACGCG 930
Qy 313 GlnAspArgLysLysSerLysTyrSerLeuValAsnValArgThrHisLysGlySer 332
Db 931 AGGACACAGAGACCGGCTTAAGTACAGGCTTGTACATAGTATGTCAGACTCCCGTGGAGCA 990
Qy 333 AspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyVal 352
Db 991 GATGATAAGCTTTCCTGTTGTTTCAAGAGCAGGATGATACAGGAGAACCCGGGTT 1050
Qy 353 SerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThr 372
Db 1051 TCGTGTGCGAAGATCTAATGCGGATTCAGGGGAAACTCTCAAAACCAATATCACTACA 1110
Qy 373 LeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuLysSerLeuValLys 392
Db 1111 TTGGTCTCTCTGTTCTACCGATAAGTAGAGCAGATCTCTCTTTATGACTCTAGTTGTG 1170
Qy 393 ArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLysLeuAlaPheGlu 412
Db 1171 AAGAAGCTCTTTAAGCGTAAAGTGAACCGTATATCCCGGATTTCAACTGCTGTTTCGAG 1230
Qy 413 HisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAsp 432
Db 1231 CATTCTCTGTATCATCTGCTGGTGAAGAGCTGTGTGATGATGATGATGATGATGATGATG 1290
Qy 433 LeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSer 452
Db 1291 CTTTACCAGTCTATGCTGAGGCTTCGAGGATGACCTCTTCATGATTTGTTGATACACATCT 1350
Qy 453 SerSerSerLeuTrpTrpGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGly 472
Db 1351 TCAGCTCTCATTTGGTATGATTTGGCTTACATTTGAACGGAAGGAGGATGCGAAGAGGT 1410
Qy 473 AspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLys 492
Db 1411 AATCGGTGTTTGGCAAAATCGGCTTCGGAAGTGGATTTAAATGTAATAGCGGATTTGGAA 1470
Qy 493 AlaLeuArgProValSerThrGluGluMetThrGlyAsnAlaTyrAlaGlySerIleAsp 512
Db 1471 GCATTAAGGCATGTG-----AAACCTTCGAACACAGCTCTCTGGGAGATTGTATTGAC 1524
Qy 513 GlnTyrProVal 516

```

```

Db 1525 AAGTATCCGGTA 1536
RESULT 11
AA23221
ID AAX23221 standard; DNA; 1611 BP.
XX AAX23221;
AC AAX23221;
XX 11-JUN-1999 (first entry)
XX A. thaliana EL5 DNA.
XX EL5; very long chain fatty acid; VLCFA; beta-keto acyl synthase;
KW plant; vegetable oil; lubricant; fuel; feedstock; plastic; cosmetic;
KW pharmaceutical; edible oil; ss.
XX Arabidopsis thaliana.
OS
XX WO9854954-A1.
XX 10-DEC-1998.
XX 01-JUN-1998; 98WO-US11384.
XX 03-JUN-1997; 97US-0868373.
XX (CRGI ) CARGILL INC.
XX (JAWO/) JAWORSKI J G.
XX (POST/) POST-BEITENMILLER MA.
XX (TODD/) TODD J.
XX Jaworski JG, Post-Beitenmiller MA, Todd J;
WPI; 1999-070227/06.
P-PSDB; AAW93431.
XX New isolated beta-keto acyl synthase polynucleotides - used
particularly for the production of transgenic plants having altered
levels of very long chain fatty acids in tissues
Claim 9; Fig 11; 76pp; English.
XX This invention describes the isolation of beta-keto acyl synthase
proteins from Arabidopsis thaliana. The products of the invention
can be used for producing vegetable oils having elevated levels of
very long chain fatty acids (VLCFA) for use as e.g. lubricants, fuels
and as a feedstock for plastics, pharmaceuticals and cosmetics. The
products can also be used for producing oils having reduced levels of
VLCFAs for use as edible oils. This sequence encodes EL5.
XX Sequence 1611 BP; 413 A; 288 C; 382 G; 528 T; 0 other;
Alignment Scores:
Pred. No.: 1-01e-151 Length: 1611
Score: 1531.50 Matches: 285
Percent Similarity: 76.20% Conservative: 96
Best Local Similarity: 57.00% Mismatches: 104
Query Match: 57.15% Indels: 15
DB: Gaps: 4
US-09-883-797-2 (1-520) x AAX23221 (1-1611)
Qy 23 ArgArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeu 42
Db 139 AGACGAAAGCTTCCTAAATTTCTTACAAAGCGTCAACATGAAATACGTCAGCTAGGTAT 198
Qy 43 HisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleIleLeuProLeuThrGly 62
Db 199 CAT-----TACCTCATTTACTCTTCCTCAAGCTCTGTTGGTTCCATTATATGGCG 249
Qy 63 ThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsn 82
Db 250 GTTTTGTACAGAGATCTCTCGATTAAACAACAGCAGCATCTTTACCAGATTG----- 303

```

```
QY 83 GlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer----- 100
Db 304 -----CITCATCTCCAATACATCATCGTGTTCATCATCTTCTCTCTCTCTTAA 351
QY 101 -----PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAsp 118
Db 352 GCTATCTTTGGCTCCACCGTGTATCATCATGAGTCGTCACAGATCTGTTTATCTCTGTTGAT 411
QY 119 PheSerCysTyrLysProGluAspGluArgLysLysSerValAspSerPheLeuThrMet 138
Db 412 TACTCTTGTTATCTCTCCGAGAGTCTTCCAGGTTAAGTATACAGAACTTATGATCAT 471
QY 139 ThrGluGluAsnGlySerPheThrAspAspThrValGlnPheGlnGlnArgLysSerAsn 158
Db 472 TCTAAGTGTGATGAAGATTTCAATGAGTCATCTTTAGAGTTTCAGAGGAAGATCTTGAA 531
QY 159 ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyLeuThrSerThrProLys 178
Db 532 CGTTCGTGGTTAGGAGAAGACTTATCTCCCTGAAGCTTTACATTTGTATCCCTCCGAGG 591
QY 179 LeuAsnMetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSer 198
Db 592 CCTACCATGATGCGGCTCTGAGGAATCTGAGCAGGTAATGTTGGTCTCTTGATAAG 651
QY 199 LeuPheGluLysThrGlyLysProAlaGluValGlyLeuLeuValLeuValAspSer 218
Db 652 CTTTTCGAGAATACCAAGATTAACCTAGGATATGTTGCTGTGTTGTTGGAATGTGAGC 711
QY 219 LeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGlu 238
Db 712 TTGTTAATCCACACCTTCGTTGTGTCAGCTATGATTGTTAACAAAGTATAAGCTTAGAGG 771
QY 239 AspIleLysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuLeuSerIleAsp 258
Db 772 AATGTTAAGAGTTTAAACCTTGTGGAATGGGTAGTCTGCTGTGTTATCTCTATCGAT 831
QY 259 LeuAlaAsnAsnLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGlu 278
Db 832 TTAGCTAAGATATGTTGCAATTCATAGGAATACATATGCTGTGTTAGTACTGAG 891
QY 279 AsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnIle 298
Db 892 AACATTACTCAGAATGTTATTTGGGAATAAGAGGCTATGTTGATCCGAATCTTTG 951
QY 299 PheArgMetGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSer 318
Db 952 TTTGCTGTGGTGTGCGGATTTGTTGCGAACAAGGGAAGATCGTAGACGCTCT 1011
QY 319 LysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsn 338
Db 1012 AAGTATAAGCTTGTTCATACCGTTAGGACTCATAAAGAGCTGTGGAAGGCTTTCAAC 1071
QY 339 CysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeu 358
Db 1072 TGTGTTTACCAAGACGAAGATGATAATGGGAAGACCGGGTTCCTGTCGNAAGATCTT 1131
QY 359 MetSerValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeu 378
Db 1132 ATGCTATAGCTGGGAAGCTCTTAAGCGGAATATCACTATTTAGGTCCTTTGGTCTT 1191
QY 379 ProLeuSerGluGlnLeuMetPheLeuSerLeuValLysArgLysMetPheLysLeu 398
Db 1192 CCTAAGTAGGAGATCTCTGTTTTCATGACTTTGTTAGGAAGAACTGTTAACTCG 1251
QY 399 LysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAla 418
Db 1252 AAGCTGAAGCGGTATATTCGGGATTTCAAGCTTGCCTTTGATCATCTTCTGATCCATGCT 1311
QY 419 GlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMet 438
Db 1312 GGTGTGAGAGCTGTGATGATGAGCTTGAGACAAGATCTGCAAGCTTTCCGACATCATGTC 1371
```

```
QY 439 GluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyr 458
Db 1372 GAGCATCCAGATGACACTGCACAGATTTGGAAACACTTCTTCAGCTCGATTTGGTAT 1431
QY 459 GluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIle 478
Db 1432 GAACTGGCTTACATAGAGGCTAAAGGTAGGATGAAGAAAGAAACCGGTTTGGCAGATT 1491
QY 479 AlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSer 498
Db 1492 GCTTTTGGAAAGTGGGTTTAAAGTGAACAGTGCAGTTCGTTGGTGGCTCTAAACAATGTC--- 1548
QY 499 ThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1549 ---AAGCCTTCGGTTAGTAGTCGTGGGAACACTGCATCGACCATATCCGGTTAAGCTC 1605

RESULT 12
AAC50224
ID AAC50224 standard; DNA; 1853 BP.
AC AAC50224;
AT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 64036.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
PD 06-SEP-2000.
PF 25-FEB-2000; 2000EP-0301439.
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
```

us-09-883-797-2.p2n.rng

Thu Feb 20 11:03:34 2003

PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	23-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	24-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0154779.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155139.
PR	08-JUL-1999;	99US-0142803.	PR	23-SEP-1999;	99US-0155486.
PR	09-JUL-1999;	99US-0142920.	PR	24-SEP-1999;	99US-0155659.
PR	12-JUL-1999;	99US-0142977.	PR	28-SEP-1999;	99US-0158458.
PR	13-JUL-1999;	99US-0143542.	PR	29-SEP-1999;	99US-0158596.
PR	14-JUL-1999;	99US-0143624.	PR	04-OCT-1999;	99US-0157117.
PR	15-JUL-1999;	99US-0144005.	PR	05-OCT-1999;	99US-0157753.
PR	16-JUL-1999;	99US-0144085.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144086.	PR	07-OCT-1999;	99US-0158029.
PR	19-JUL-1999;	99US-0144325.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144331.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144334.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159329.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159637.
PR	21-JUL-1999;	99US-0144814.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0145086.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	22-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161922.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147302.	PR	29-OCT-1999;	99US-0162142.

Alignment Scores:

```

Pred. No.: 1.25e-151 Length: 1853
Score: 1531.50 Matches: 285
Percent Similarity: 76.20% Conservative: 96
Best Local Similarity: 57.00% Mismatches: 104
Query Match: 57.15% Indels: 15
DB: 21 Gaps: 4

US-09-883-797-2 (1-520) x AAC50224 (1-1853)

QY 23 ArgArgArgLeuProAspLeuThrSerValLysLeuLysTyrValLysLeuGlyLeu 42
Db 230 AGACGAAGCTTCCTAAATTTCTTACAAACGCTCAACATCAAGTACGTAAGTAT 289
QY 43 HisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleIleLeuProLeuThrGly 62
Db 290 CAT-----TACCTCATCTACTCATCTCTTCAAGCTCTGTTGGTTCCTCAATTAATGCG 340
QY 63 ThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTyrSerAsn 82
Db 341 GTTTTGTCTACAGAGATCTCTCGATTAAACAACAGACGATCTTACCAGATTGG----- 394
QY 83 GlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer----- 100
Db 395 -----CTTCATCTCCAATACATCTCTGCTTTCATCTCTTCTCTGCTTTA 442
QY 101 -----PheValLeuThrLeuThrValAlaAsnArgSerLysProValTyrLeuValAsp 118
Db 443 GCTATCTTTGGCTCCACCGTTTACATCATGAGTGTCCAGATCTGTTTATCTCGTGTAT 502
QY 119 PheSerCysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMet 138
Db 503 TACTCTGTATCTCTCCGGAGAGTCTTCAGGTTAAGTATCAGAAAGTTATGATCAT 562
QY 139 ThrGluGluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsn 158
Db 563 TCTAAGTTGATTGAAGATTTCATAGTATCTTTAGAGTTTCAGAGAAAGATTCTTGAA 622
QY 159 ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerProProLys 178
Db 623 CTTTCGGTTTGGTAAAGAGAGACTTATCTCCCTGAAGCTTTACATTTGATCCCTCCGAGG 682
QY 179 LeuAsnMetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSer 198
Db 683 CCTACGATGATCGCGCTCGTGAGGAATCTGACGAGTAAATGTTGGTCTCTGTATAG 742
QY 199 LeuPheGlyLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSer 218
Db 743 CTTTCGGAATACCAAGATTAAACCTTAGGATATTGGTGTGTGTTGTTGTAATTGTAGC 802
QY 219 LeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGlu 238
Db 803 TTGTTTAAATCCACACCTTCGTTGTCAGCTATGTTGTTTAAACAGTAAAGCTTAGAGG 862
QY 239 AspIleLysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAsp 258
Db 863 AATGTTAAGATTTTAACTTGGTGAATTTGGGTGAGTGTGCTGTTTATCTATCATCAT 922
QY 259 LeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGlu 278
Db 923 TTAGCTAAAGATATGTTCAAGTTCATAGGAATACCTTATGCTGTGTGTTAGTACTGAG 982
QY 279 AsnIleThrLeuAsnThrTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIle 298
Db 983 AACATTACTCAGAATTGTTATTTTGGGAATAAGAGGCTATGTTGATCCGATTTGTTG 1042
QY 299 PheArgMetGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSer 318
Db 1043 TTTTCGGTGTGTTGGTGGGATTTTCTGTGCAACAGGCGGAAAGATCGTAGACGGTCT 1102
QY 319 LysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsn 338
Db 1103 AAGTATAAGCTTGTTCATACCGTTAGGACATCAAGAGAGCTGTTGAGAGAGGCTTTCAAC 1162

```

```

QY 339 CysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeu 358
Db 1163 TGTGTTTACCAGACCAAGATGATAATGGGAAGACCGGGTTTCGTTGTCGAAGATCTT 1222
QY 359 MetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeu 378
Db 1223 ATGGCTATAGCTGGGAAGCTCTTAAGCGGAATATCACTACTTCTAGGCTCTTGGTCTT 1282
QY 379 ProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu 398
Db 1283 CCTAATAGTCAGCAGATCTCTGTTTTCATGACTTTGGTTACGAAGAACTGTTTAACTCG 1342
QY 399 LysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAla 418
Db 1343 AAGCTGAAGCGGTATATTCGGATTCAAGCTTGGTTTGATCATTTCTGTATCATCATGCT 1402
QY 419 GlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTyrIleHisMet 438
Db 1403 GGTGGTAGAGCTGTGATTGATGAGCTTGAGAAGAACTCTGCAGCTTCCGACACTCATGTC 1462
QY 439 GluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrPyr 458
Db 1463 GAGGCACTCAGAAATGACACTGCACAGATTGGAAACACTTCTTCGAGCTCGATTGGTAT 1522
QY 459 GluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIle 478
Db 1523 GAACCTGGCTTACATAGAGGCTAAAGGTAGGATGAAGAAAGAAACCGGTTTGGCAGATT 1582
QY 479 AlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSer 498
Db 1583 GCTTTTGGAGTGGGTTTAAAGTAAACAGTGCAGATTGGTGGTCTCTAAACAATGTC--- 1639
QY 499 ThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
Db 1640 ---AAGCCTCTGGTTAGTAGTCGTTGGGAACACTGCATCGACCATATCCGGTTAAGCTC 1696
RESULT 13
AAT04124
ID AAT04124 standard; cDNA to mRNA; 1783 BP.
XX AAT04124;
AC AAT04124;
XX DT
XX DT
XX DT
DE Jojoba wax-synthase cDNA clone pCGN7614.
XX Max-synthase; long-chain alcohol-fatty-acyl-transferase; wax ester;
XX Jojoba; oilseed; transgenic plant; crop improvement; Brassica; ds.
XX Simmondsia chinensis.
XX Key Location/Qualifiers
XX CDS 10..1575
XX /*tag= a
XX /EC_number= 2.3.1.75
XX US4445947-A.
XX 29-AUG-1995.
XX 20-NOV-1991; 91US-0796256.
XX 20-MAY-1993; 93US-0066299.
XX 20-NOV-1991; 91US-0796256.
XX 21-AUG-1992; 92US-0933411.
XX 13-NOV-1992; 92WO-0509863.
XX (CALJ ) CALGENE INC.
XX Lardizabal KD, Lassner MW, Metz JG;
XX WPI; 1995-310894/40.

```

DR P-PSDB; AAR79923.

XX DNA construct expressing jojoba wax synthase and transformed

PT Brassica cells - useful for producing wax ester(s) for use in

PT pharmaceuticals and cosmetics, etc

XX Claim 1; Column 49-54; 50pp; English.

XX 2 Wax synthases were isolated from a jojoba microsomal membrane prepn.

CC and tryptic fragments were sequenced (AAR79923-42). The sequence

CC information was used to design oligonucleotide probes for screening

CC jojoba embryo cDNA libraries. A 1.5 kb clone was isolated and

CC additional sequences were identified by 5'RACE or by rescreening.

CC Clone PCGN7614 was obt'd. (AAT04124) that encoded wax-synthase, and

CC was used to construct plasmids for transformation of plants.

XX Sequence 1783 BP; 450 A; 446 C; 432 G; 455 T; 0 other;

XX

Alignment Scores:

Pred. No.:	2,19e-150	Length:	1783
Score:	1519.50	Matches:	284
Percent Similarity:	75.30%	Conservative:	88
Best Local Similarity:	57.49%	Mismatches:	115
Query Match:	56.70%	Indels:	7
DB:	16	Gaps:	4

US-09-883-797-2 (1-520) x AAT04124 (1-1783)

QY 26 LeuProAspLeuThrSerValLysLeuLysThrValLysLeuGlyLeuHisAsnSer 45

Db 85 CTCGCCAATCAAGTCTCTCATCACTACACGCTCAGCTCGGTACCAC----- 138

QY 46 CysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrValLeu 65

Db 139 ---TACTTAATCTCAATGCCCTCTCTCTCGTATTCATCCCTTTTGGGCTCGCTCG 195

QY 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85

Db 196 GCCCACCTCTCTCTCTCGGCCCATGACTGTGCTCGCTCTCTC-----GACCTCTCT 249

QY 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105

Db 250 CGCCGCAACCT 309

QY 106 TyrValAlaAsnArgSerLysProValThrLeuValAspPheSerCysThrLysProGlu 125

Db 310 CATTTCTTGACCGCCCT 369

QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145

Db 370 CGGAACCTGATAACATCCACGAGATGTTTCATGGACCGGACCTCTCTCTCTCTCTCT 429

QY 146 ThrAspAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAspGlu 165

Db 430 TCTAAGGAGAAATATTGAGTTTCAGAGAAAGATCTTGGAGAGGCGCGGTATGGCCGGGAA 489

QY 166 ThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAlaArg 185

Db 490 ACTTACGTCCTCCGATCCGCTACTAGTTCCTCCGCGGCGGAGCATAGCAGCAGCAGG 549

QY 186 AlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGlyThrGlyLe 205

Db 550 GCCGAGCGGAGGAGGTATGTACGGGGCGATCGAGAGGTGTGGAGAGACCGGGGTG 609

QY 206 LysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThrProSer 225

Db 610 AAGCCCAAGCAGATAGATAGTGGTGGTGAACGCTGAGCTGTGTTAACCCCAACCGCTCG 669

QY 226 LeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeu 245

Db 670 CTGTATCCATGATAGTAACTTACAACTTACAGGCTTACAGGCTTATATCTAGTATATCT 729

QY 246 GlyGlyMetCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLeuLys 265

Db 730 GGTGGCATGGTTCAGTGTGGCTCATTTCCATTGATCTTGCACAGACCTCTCTACAG 789

QY 266 AlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyr 285

Db 790 GTTTACCGTAACACATATGTGTAGTAGTGAGCAGAAACATGACCCCTTAATGGTAC 849

QY 286 PheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAla 305

Db 850 TGGGCAATGACCGCTCCATGCTTATCACCACCTGCTATTTTCGATGGTGGCTGCC 909

QY 306 IleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuValAsnVal 325

Db 910 ATCATCTCTCAACCGCTGGGTGATGTCGCCGATCCCAAGTACCACTCTTACACA 969

QY 326 ValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAsp 345

Db 970 GTACGCCACCAAGGGCGCTGACGACAAGTCTCTATAGATGCGCTCTACAAACAAGAT 1029

QY 346 GluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAla 365

Db 1030 GAAATAACAAGTAGTGTGCTTATCAAGATGACGAACTGATGGCAGTGCCTGAAGCC 1089

QY 366 LeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMet 385

Db 1090 CTAAGGCCACACATCAGACCTTGGTCTCTGCTCCCATGTCAGAACACTCTCTC 1149

QY 386 PheLeuIleSerLeuValLysArgLysMetPheLysLeu---LysValLysProTyrIle 404

Db 1150 TCTTTGCCACCTTAGTGGCACCTAAGTCTTCAAGATGACGAACTGAAAGCCATCATC 1209

QY 405 ProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeu 424

Db 1210 CCAGATTCAAGTTGGCAGCAAGCACTTCTGATCTCATGAGGAGGCAAGCAGCTGTG 1269

QY 425 AspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMetThr 444

Db 1270 GATGAGCTCGAGAGCAACTTGGAGTTCAGCCCATGGCACCTGAACCTCGAGGATGACA 1329

QY 445 LeuHisArgPheGlyAsnThrSerSerSerSerSerSerSerSerSerSerSerSer 464

Db 1330 CTGTATAGTATTGGAAACACATCGATGAGTCTCATTTGGTATGGATTTGGTTCAGGTTTC 1389

QY 465 AlalysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGlyPhe 484

Db 1390 GCAAAAGGAGGATCCCGTAAGGCTGATCGAATTTGGATTTGGATTTGGTTCAGGTTTC 1449

QY 485 LysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThrGly 504

Db 1450 AAGTGTAAACAGTGTGTGTGGAGGCTTTGAGGAGTGTCAATCCCGCTAGA---GAGAAG 1506

QY 505 AsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518

Db 1507 AATCTTTGGATGGATGAATTAAGAAATTTCCTCTGTCATGTG 1548

RESULT 14

AAQ90208

ID AAQ90208 standard; cDNA; 1783 BP.

XX AAQ90208;

XX 04-DEC-1995 (first entry)

XX Jojoba fatty acyl-CoA cytoplasmic protein cDNA in PCGN7614.

XX very long chain fatty acid; fatty acyl-CoA; ss.

XX Jojoba.

XX Key

XX Location/Qualifiers

XX 10..1575

XX CDS

XX /*tag= a

Thu Feb 20 11:03:34 2003

```

|||||
Db 1244 TTGGTCTCTTGTCTACCGATAAGTGCAGATCTCTTCTTTATGACTCTAGTTGTG 1303
QY 393 ArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLysLeuAlaPheGlu 412
Db 1304 AAGAGCTCTTTAACGGTAAAGTGAACCGTATATCCCGGATTTCAAACTTGCTTTCGAG 1363
QY 413 HisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAsp 432
Db 1364 CATTTCTGTATCCATGCTGGTGAAGAGCTGTGATCGATGAGTTAGAGAGATCTGCAG 1423
QY 433 LeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSer 452
Db 1424 CTTTCACCAAGTTCATGTCGAGGCTTCGAGGATGACTCTTCATCGATTTGGTAAACATCT 1483
QY 453 SerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGly 472
Db 1484 TCGAGCTCCATTTGGTATGAAATTTGGCTTACATTGAAGCGAAGGAGGATCGGAAGAGGT 1543
QY 473 AspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLys 492
Db 1544 AATCGTGTGTGGCAATCGGTTCCGAAGTGGATTTAAATGTAATAGCGGATTTGGGAA 1603
QY 493 AlaLeuArgProValSerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAsp 512
Db 1604 GCATTAAGGCATGTG-----AAACCTTCGACAACAGCTCTTGTGAAGATTGTATTGAC 1657
QY 513 GlnTyrProVal 516
Db 1658 AAGTATCCGGTA 1669

```

Search completed: February 19, 2003, 09:25:13
Job time : 342 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 10:27:18 : Search time 131 Seconds
(without alignments)

2021.743 Million cell updates/sec

Title: US-09-883-797-2

Perfect score: 2680

Sequence:

1 MDRERLTAFAFRDSSSAVI.....EMTGNAGSIDQIPVKVVQ 520

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:

424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+pn2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09883797/runat_14022003_102503/app_query.fasta_1.711
-DB=PublishedApplications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=ptc -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -NODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09883797 -CGN_1_1_80 -runat_14022003_102503_19605
-NCPU=6 -ICPU=3 -NO_XLPX -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA:

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2680	100.0	1560	10	US-09-883-797-1
2	2680	100.0	1563	9	US-09-938-842A-1552
3	1639	61.2	1530	9	US-09-938-842A-1205
4	1588.5	59.3	1587	9	US-09-938-842A-1598

5	1563	58.3	1548	10	US-09-883-797-13
6	1531.5	57.1	1611	10	US-09-883-797-9
7	1441	53.8	1650	10	US-09-883-797-7
8	1438.5	53.7	1491	10	US-09-892-325-3
9	1438.5	53.7	1494	9	US-09-938-842A-569
10	1438.5	53.7	1502	10	US-09-883-797-11
11	1438.5	53.7	1807	10	US-09-892-325-2
12	1438.5	53.7	3722	10	US-09-892-325-1
13	1438	53.7	1653	9	US-09-938-842A-2597
14	1323.5	49.4	1512	10	US-09-883-797-5
15	1317.5	49.2	1521	10	US-09-877-476-37
16	1314.5	49.0	1521	10	US-09-877-476-23
17	1313.5	49.0	1521	10	US-09-877-476-41
18	1310.5	48.9	1521	10	US-09-877-476-15
19	1308.5	48.8	1521	10	US-09-877-476-39
20	1307.5	48.8	1521	10	US-09-877-476-21
21	1306.5	48.8	1521	10	US-09-877-476-31
22	1306.5	48.8	1524	10	US-09-877-476-33
23	1303.5	48.6	2782	10	US-09-905-657-1
24	1302.5	48.6	1521	10	US-09-877-476-19
25	1302.5	48.6	1709	10	US-09-877-476-1
26	1301.5	48.6	1521	10	US-09-877-476-1
27	1300.5	48.5	1521	10	US-09-877-476-25
28	1300	48.5	1518	10	US-09-877-476-13
29	1299.5	48.5	1521	10	US-09-877-476-7
30	1299.5	48.5	1524	10	US-09-877-476-3
31	1299.5	48.5	1709	10	US-09-877-476-35
32	1298	48.4	1479	10	US-09-883-797-3
33	1296.5	48.4	1521	10	US-09-877-476-27
34	1295.5	48.3	1521	10	US-09-877-476-11
35	1295.5	48.3	1521	10	US-09-877-476-29
36	1294	48.3	1736	10	US-09-877-476-5
37	1293	48.2	1518	10	US-09-877-476-9
38	958	35.7	1431	9	US-09-938-842A-1987
39	528.5	19.7	811	10	US-09-770-445-774
40	501	18.7	409	10	US-09-878-574-4051
41	460	17.2	468	10	US-09-770-444-253
42	427	15.9	387	10	US-09-878-574-1065
43	401	11.2	343	10	US-09-878-574-2604
44	295	11.0	276	10	US-09-878-574-12488
45	160	6.0	1359	10	US-09-837-654-2

ALIGNMENTS

RESULT 1
US-09-883-797-1
; Sequence 1, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-1
Alignment Scores:
Pred. No.: 3.78e-313
Score: 2680.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 1560
Matches: 520
Conservative: 0
Mismatch: 0
Indels: 0

DB: 10 Gaps: 0

US-09-883-797-2 (1-520) x US-09-883-797-1 (1-1560)

QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgSerSerSerAlaValile 20
Db 1 ATGGATCGAGAGATTAAACGGCGAGATGGCGTTTCGAGATTCAATCATCGCGCGTTATA 60
QY 21 ArgIleArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeu 40
Db 61 AGAATTTCGAAGACGTTTGGCGGATTATTAACCGTCCGTTAAGCTCAAAATACGTGAAGCTT 120
QY 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuLleLeuLeuProIeu 60
Db 121 GGACTTCACAACCTTCGCAACGTCACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTyr 80
Db 181 ACCGGAACCGTGTGTTACGCTAACCGGCTAACCGGCTAACCGGCTAACCGGCTAACCGGCT 240
QY 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100
Db 241 TCTAACCGCGGTTCAACTCGACACGCGACGAGACTTACCTGCTTGGTTTCTCTCTCTCC 300
QY 101 PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSer 120
Db 301 TTCGTTTTCACCTCTACGTTGGCTAACCGGCTAACCGGCTAACCGGCTAACCGGCTAACCGG 360
QY 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140
Db 361 TGCTACAAACCGGAAGACGAGCGTAAATATACAGTAGATTCTGTCGACGATGACTGAG 420
QY 141 GluAsnGlySerPheThrAspThrValGlnPheGlnGlnArgIleSerAsnArgAla 160
Db 421 GAAATGATCATTCACCGATGACACGCTTTCAGTTCCAGCAAGAAATCTCGAACCGGGCC 480
QY 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsn 180
Db 481 GGTTTGGGAGACGAGACGATCTCGCCACGTCGCATTAACCTCAACGCCCGCGAAGCTAAAT 540
QY 181 MetSerGluAlaArgAlaGluAlaGluValMetPheGlyAlaLeuAspSerLeuPhe 200
Db 541 ATGTCAGAGGACGTCGCGAAAGCTGAAGCGGTTATGTTGGAGCGCTTAGATTCCCTCTTC 600
QY 201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
Db 601 GAGAAACCGGAATTAACCGCGCAAGTCGGAATCTTCATAGTAACCTGCAGCTTATTC 660
QY 221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
Db 661 AATCCGACGCGCTCTATCAGCGATGATCGTGAACCATTAAGAATGAGAGAGACATC 720
QY 241 LysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla 260
Db 721 AAAAGTTACAACTCGGAGGATGGGTTCTCCGCGGATTAATCTCAATCGATCTCGCT 780
QY 261 AsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIle 280
Db 781 ACAATCTCTCAACCAACCAACCTAATCTTACGCTCTCTGTTGAAGCAACGGAACATA 840
QY 281 ThrLeuAsnTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg 300
Db 841 ACCCTAACTGTGTACTTCGGAATGACCGGCTCAATGCTCTCTCGCAACTGCATCTCCGA 900
QY 301 MetGlyGlyAlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyr 320
Db 901 ATGGGCGGAGCTCGGATCT 960
QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
Db 961 TCGCTGGTCAACCTCGTTCAACACATATAAGGATCAACGACCAAGAACTCAATTCGCTG 1020
QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360

Db 1021 TACCAGAGAGAGACGAGAGAGAAATCGGTGTCTCTTTAGCTAGAGAGCTCATGTCT 1080
QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeu 380
Db 1081 GTCCGCGAGAGCGCTCTGAAAACAAACATACGACTTTTAGGACGATGTTCTTCCATTC 1140
QY 381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
Db 1141 TCAGAGCAGTTGATGTTCTTGGTTCCCTTGGTCAAAAGGAAGATGTTCAAGTTAAAGTT 1200
QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
Db 1201 AAACCGTATATTCGCGATTCAAGCTAGCTTTTCGACATTTCTGTATTCACGCGAGGAGT 1260
QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTyrHisMetGluPro 440
Db 1261 AGAGCGGTTCTAGACGAAGTGCAGAAATCTTGATCTCAAGATTTGGCACATGGAACCT 1320
QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTyrGluMet 460
Db 1321 TCTAGATGACTTTGCACAGATTTGCTAACACTTCGAGTAGCTCGCTTTGGTATGAGATG 1380
QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTyrGlnIleAlaPhe 480
Db 1381 GCTTATACCGAAGCTAAGGTCGGGTTAAAGCTGGTGACCGACTTTGGCAGATTCGCTT 1440
QY 481 GlySerGlyPheLysCysAsnSerAlaValTyrLysAlaLeuArgProValSerThrGlu 500
Db 1441 GGATCGGTTTCAAGTGTATAGTTCGGTTTGGAAAGCGTTACGACCGGTTTCGACGGAG 1500
QY 501 GluMetThrGlyAsnAlaTyrAlaGlySerIleAspGlnTyrProValLysValGln 520
Db 1501 GAGATGACCGGTTAATGCTTGGCTGTTTCGATTCATCAATATCCGTTTAAAGTTGTGCA 1560

RESULT 2

US-09-938-842A-1552
; Sequence 1552, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1552
; LENGTH: 1563
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1552

Alignment Scores:
Pred. No.: 3.8e-313 Length: 1563
Score: 2680.00 Matches: 520
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-883-797-2 (1-520) x US-09-938-842A-1552 (1-1563)

QY 1 MetAspArgGluArgLeuThrAlaGluMetAlaPheArgAspSerSerSerAlaValile 20


```

Db 1 ATGGATCGAGAGATTAACCGCGAGATGGCTTTCGAGATTCATCATCGCGCGTTATA 60
QY 21 ArgIleArgArgLeuProAspLeuThrSerValLysLeuLysTyrValLysLeu 40
Db 61 AGAATTCGAAGACGTTTTCGGGATTTATTAACGTCGCTTAAGCTCAATAGTGAAGCTT 120
QY 41 GlyLeuHisAsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeu 60
Db 121 GGACTTCACAACCTTCGACAGTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 61 ThrGlyThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrp 80
Db 181 ACCGGAACCGTGTCTGCTTACGTAACCGGCTTAACGTCGATGCTTCTGAGCTTTGG 240
QY 81 SerAsnGlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer 100
Db 241 TCTAACCGAGCGGTTCACTCGACACGCGCAGCAGACTTACCTGCTTGGTTTCTCTCC 300
QY 101 PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAspPheSer 120
Db 301 TTCGTTTTGACCTCTACGTTGGCTAACCGGCTTAACCGGTTTACCTAGTGGATTTCTCC 360
QY 121 CysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMetThrGlu 140
Db 361 TCCTACAAACCGGAGACGAGCGTAAATATCATAGTATCGTTCTTACGATCATCTGAG 420
QY 141 GluAsnGlySerPheThrAspThrValGlnPheGlnArgIleSerAsnArgAla 160
Db 421 GAAAAATGGATCATTCACCGATCACAGGTTTCAGTTCCAGCAAGAATCTCGAACCGGGCC 480
QY 161 GlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsn 180
Db 481 GTTTTGGGAGACGACGATATTCGACGTCGATTAATCAACGCCCCCGGAGCTTAAT 540
QY 181 MetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPhe 200
Db 541 ATGTCAGAGGACGTCGCGAAGCTGACCGGTTATGTTGGAGCCCTTAGATTCCCTCTTC 600
QY 201 GluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPhe 220
Db 601 GAGAAACCGGAATTAACCGCGGAAAGTCGGAATCTTGATTAACCTGACGTTATTC 660
QY 221 AsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIle 240
Db 661 AATCCGAGCGGCTCTATCATCAGGATGATCGTGAACCATTAACAGATGAGAGAGACATC 720
QY 241 LysSerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAla 260
Db 721 AAAAGTTACAACTCCGAGGAATGGTTGCTCCGCGGATTAATCTCAATCATCTCGCT 780
QY 261 AsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIle 280
Db 781 AACAACTCTCTCAAGCAACCCCTTAATCTTACGCTGTCGTTGAGCAACGCAAAACATA 840
QY 281 ThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArg 300
Db 841 ACCCTAACTGGTACTTCGGAATGACCGGCTCAATGCTCTCTGCACTGCTATCTCCGA 900
QY 301 MetGlyClyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyr 320
Db 901 ATGGCGGAGCTCGGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 321 SerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysVal 340
Db 961 TCGCTGCTCAACGCTGTTGGAACACATAAAGGATCAGACGACAGAACTACAATTCGCTG 1020
QY 341 TyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSer 360
Db 1021 TACCAAGAGGAGACGAGAGGAGCAATCGGTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 361 ValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeu 380

```

```

Db 1081 GTCGCGGACGCTCTGAAACAAACATCACGACTTTAGACCGATGTTCTTCCATTG 1140
QY 381 SerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysVal 400
Db 1141 TCAGAGCAGTTGATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 401 LysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGly 420
Db 1201 AAACCGTATATTCGGATTTCAAGCTAGCTTTCGAGCATTTCTGTATTTCAGCAGAGGT 1260
QY 421 ArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTyrPheHisMetGluPro 440
Db 1261 AGAGCGGTTCTAGCAAGTGCAGAAAGTCTTGTATCTCAAGATTTGGCAGATGGAACCT 1320
QY 441 SerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerSerLeuTyrTrpGluMet 460
Db 1321 TCTAGAAACGCTTTCACAGATTTGGTAACACTTCAGTAGCTCGCTTTCGTATGAGATG 1380
QY 461 AlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPhe 480
Db 1381 GCTTATACCGAAGCTAAGGTCGGGTTAAAGCTGGTGACCGACTTTGGCAGATTCGCTTT 1440
QY 481 GlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGlu 500
Db 1441 GGATCGGTTTCAAGTGAATAGTGGGTTTGGAAAGCGTTACGACCGGTTTCGACGGAG 1500
QY 501 GluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysValValGln 520
Db 1501 GAGATGACCGGTAATGCTTGGCTGGTTCGATTGATCAATAATCCGGTTAAAGTTGTCAA 1560

```

```

RESULT 3
US-09-938-842A-1205
; Sequence 1205, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1205
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1205

```

```

Alignment Scores:
Pred. No.: 1,25e-187 Length: 1530
Score: 1639.00 Matches: 304
Percent Similarity: 78.38% Conservative: 84
Best Local Similarity: 61.41% Mismatches: 101
Query Match: 61.16% Indels: 6
DB: 9 Gaps: 3
US-09-883-797-2 (1-520) x US-09-938-842A-1205 (1-1530)

```

```

QY 24 ArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHis 43
Db 43 CGTATCTACCTGATTTCAAAAAATCAGTGAAGCTTAAATATGTGAAGCTTGGTTACCAT 102
QY 44 AsnSerCysAsnValThrThrIleLeuPhePheLeuIleLeuProLeuThrGlyThr 63

```


Db 706 ATGGTGATAAACCATTACAGATGAGAGGAACATACCTTAGTTACAACTTGGAGGATG 765
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 249 GlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLeuLysAlaAsnPro 268
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 766 GGATGTCGGCTGGAATCATAGTATGATGCTGCTGCGACATGCTTCTAGTCTAACCT 825
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 269 AsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsn 288
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 826 AATAGTTATGCTGTTGTTGAGTACTAGATGGTGGGTATATATGGTACGTGGGAAGT 885
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 289 AspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeu 308
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 886 GACAAGTCAATGTTATCACTAATCTTTCTTAGGATGGTGTCTGCGGTATGCTC 945
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 309 SerAsnArgGlnAspArgLysSerLysTyrSerLeuValValValValValThr 328
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 946 TCTAACCGCTGCTGCTGCTTCCGCTACGCTAGTACCGCTCTCGAGCACATTTGCCGAAT 1005
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 329 HisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGly 348
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1006 CATAAGCTGCTCAGCACCTGAGCTTCAGGAGTGTGTACCAGGAAGAGATGAACAAGGA 1065
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 349 ThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThr 368
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1066 TTCAAGGGGTGAAGATAGAGACTTAATGAAGTTGGAGTGAAGCTCTCAAGACA 1125
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 369 AsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIle 388
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1126 ACATCACTACCTTAGTCTCTTGTCTACCTTTCTCCGAGCAGCTTCTCTCTTCT 1185
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 389 SerLeuValLysArg----- 393
Db 1186 GCATTGTCGCGCCGAACATTCTACCTCTGCCAAAGCTCCACCAACCCTTCTCTCT 1245
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 394 -----LysMetPheLysLeuLys-----ValLysPro 402
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1246 ACTTCGCGCCACCGCAAAACCAATGGAATCAAGTCTTCTCTTCGATGTCCTCAAGCCA 1305
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAla 422
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1306 TACATCCGGGACTACAAGCTCGCTTCGAGCATTTTGTCTCCACGCGGCAAGCAAGTA 1365
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1366 GTGCTTGAAGAGCTTCAAAAGCAATCTAGCTTGAAGTGAAGAGATATGAGGCTTCTAGG 1425
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1426 ATGACACTCACAGCTTTGGAAACACTTCTAGCAGTGGAACTCTGTATGATGGCTTAC 1485
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1486 ATGGAGGCCAAGAAAGTGTTCGTAGAGCGATAGGGTTGGCAGATCGCTTTCGGTCT 1545
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 1546 GGTTTTAAGTGTACAGCTGTGTGTGGAAGGCAATGAGGAGGTGAAG---AAGCCAACC 1602
Qy |||||.....|||||.....|||||.....|||||.....|||||.....|||||.....
Db 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 1603 AGGAACAATCTTGGTGGATTGCATCAACCGTTACCCCTGTG 1644
RESULT 8
US-09-892-325-3
; Sequence 3, Application US/09892325
; Patent No. US20020116735A1
; GENERAL INFORMATION:
; APPLICANT: Kunst et al.
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
; Involved In Very Long Chain Fatty Acid Synthesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell
Leigh & Whinston, LLP
STREET: One World Trade Center, Suite
1600, 121 S.W. Salmon Street
CITY: Portland
STATE: OR
COUNTRY: USA
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.5-inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,325
FILING DATE: 26-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/058,947
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: David J. Earp, Ph.D.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5493-50032/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-892-325-3
Alignment Scores:
Pred. No.: 1,8e-163 Length: 1491
Score: 1438.50 Matches: 279
Percent Similarity: 74.49% Conservative: 89
Best Local Similarity: 56.48% Mismatches: 113
Query Match: 53.68% Indels: 13
Gaps: 6
US-09-883-797-2 (1-520) x US-09-892-325-3 (1-1491)
Qy 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45
Db 16 ATGCAGAGTTCTCTAGCTCGGTGAAGCTCAAGTACGTAAGTGGTTACCAATATTG 75
Qy 46 CysAsnValThrIleLeuPhePheLeuIleLeuLeuProLeuThrGlyThrValLeu 65
Db 76 GTTAAC-----CATTTCTTGAGTTTCTTTTGATC---CCGATCATGGCTATTGTCCGC 126
Qy 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85
Db 127 GTTGAGCTTCTCGGATGGTCTGAAGAGATCTTAATGTTTGGAAAT-----TCACTC 180
Qy 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
Db 181 CAGTTTGACCTAGTTCAGGTTCTATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 240
Qy 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
Db 241 TACTTCATGTCACAGCCAGCCACCATCTACCTCGTTGACTATTCTTGTAAAGCCACCT 300
Qy 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
Db 301 GTCAGGTGTCTGTCTC-----CCCTTCGCAACTTTCATGGAACACTCTCGTTGATC 351
Qy 146 ThrAspAsp-----ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeu 162
Db 352 CTCAGGACAAAGCCCTAAGAGCGTCGAGTTCCAAATGAGAATCCTTGAACGTTCTTGGCCTC 411

QY 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
 DB 412 GGTGAGGAGACTGTCTCCCTCCGCTATTTCATTATATATTCCTCCACACCAACCATGGAC 471
 QY 183 GluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
 DB 472 GCGGCTAGAACGCGCTCAGATGGTATCTTCGAGGCCATGACCATCTTTTCAGAAA 531
 QY 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
 DB 532 ACCGGCTTAACCTTAAGACCTGACATCCCTATCTGTCACCTGCTCTCTCTCTCTCC 591
 QY 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgLysAspIleLysSer 242
 DB 592 ACACCATCGCTCAGCTATGGTCAATCAACAATAATAGCTTAGGAGTAATATCAAGAGC 651
 QY 243 TyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
 DB 652 TTCATCTTTTGGGGATGGCTGACGCGGGCTGATCTCAGTTCATCTAGCCCGGAC 711
 QY 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
 DB 712 TTGCTCAAGTTCATCCCAATTCAAATGCAATCATCTGTCAGCAGCGGATCATACGCCT 771
 QY 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
 DB 772 AATTACTATCAAGCAACGAGAGCCATGTTGTTACCAATGTCTCTCCGATGGGT 831
 QY 303 GlyAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeu 322
 DB 832 GCGGACGCCATPACATGTCAACCGCGGCTGACCGGTCGCGGAGCAATACAAAGCTT 891
 QY 323 ValAsnValValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGln 342
 DB 892 TCCACCTCGTCCGGACACACCGTGGCGCTGACGACAAGTCTTCTACTGTGTCTACGAA 951
 QY 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
 DB 952 CAGGAGACAAAGAGACACGTTGGCATCAACTGTGTCACCAAGATCTCATGGCCATCGCC 1011
 QY 363 GlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGlu 382
 DB 1012 GGTGAAGCCCTCAAGGCAACATCACCACAATAGTCTCTTGGTCTACCGGCGTCAGAA 1071
 QY 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
 DB 1072 CAACTTCTCTCTCAGCTCCCTAATCGGAGCTAAATCTTCAACCCGAAATGGAAACCA 1131
 QY 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyArgAla 422
 DB 1132 TACATACCGGATTTCAAGCTGGCTTCCGACACATTTGTCATTCAGCAGGAGGAGCGG 1191
 QY 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
 DB 1192 GTATCGACGAGCTCCAAAAGAAATCTCAACTATCAGAGAACACGTTGAGGCGCTCAAGA 1251
 QY 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTrpGluMetAlaTyr 462
 DB 1252 ATGACACTACATCGTTTGTGAACACGCTCATCTTCATGTTATGTTAGGAGCTTAGCTAC 1311
 QY 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
 DB 1312 ATGAGTCTAAAGGAGAAATGAGGAGAGGCGATCGCGTTTGGCAAAATCGCGTTTGGGAGT 1371
 QY 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
 DB 1372 GGTTCAGGTCAACTCTCGCGTGTGGAAATGTAACTGACGATTAACACACCTTAAG --- 1428
 QY 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
 DB 1429 ---GACGGACCATGGTCCGATTGTATCGACCGTTACCTGTC 1467

RESULT 9

US-09-938-842A-569
 ; Sequence 569, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN
 ; FILE REFERENCE: SCRIP1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 569
 ; LENGTH: 1494
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-569

Alignment Scores:

Pred. No.: 1-8e-163 Length: 1494
 Score: 1438.50 Matches: 279
 Percent Similarity: 74.49% Conservative: 89
 Best Local Similarity: 56.48% Mismatches: 113
 Query Match: 53.68% Indels: 13
 DB: 9 Gaps: 6

US-09-883-797-2 (1-520) x US-09-938-842A-569 (1-1494)

QY 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45
 DB 16 ATCCGAGGTTCTAGCTCGGTGAAGCTCAAGTACGTGAAGCTTGGTTAGCAATATTG 75
 QY 46 CysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrValLeu 65
 DB 76 GTTAAC-----CATTCCTTGAGTTTCTTTTGATC---CCGATCATGGCTATTGTCGCC 126
 QY 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85
 DB 127 GTGAGCTTCTTCGGATGGGTCTGGAAGAGATCCTTAATGTTGGAAT-----TCACCTC 180
 QY 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
 DB 181 CAGTTTGACCTAGTTCAGGTTCTATGTTCTTCCTTCTTCATCTTCATCTCCACTGTT 240
 QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
 DB 241 TACTTTCATGTCACGACGACCATCTACCTCGTTGACATCTCTTGTGTACAGCCACT 300
 QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
 DB 301 GTCAGGTGTCTGTCTC-----CCCTTCGCAACTTTCATGGAACACTCTCGTTTGATC 351
 QY 146 ThrAspAsp-----ThrValGlnPheGlnGlnArgIleSerAsnArgAlaGlyLeu 162
 DB 352 CTCAGGACACGCTAAGAGCTGAGTTCCTCAAAATGAGAAATCTTGAACGTTCTGGGCTC 411
 QY 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
 DB 412 GGTGAGGAGACTGTCTCCCTCGGCTATTTCATTATATTCTCCACCAACCATGGAC 471
 QY 183 GluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
 DB 472 GCGGCTAGAACGAGGCTCAGATGGTATCTTCGAGGCCATGGACGATCTTTTCAAGAAA 531

```

QY 203 ThrGlyLeuLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 532 ACCGGTCTTAAACCTAAAGAGCTCGACATCTTATCGCAACTGCTCTCTTCTCTCC 591
QY 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
Db 592 ACACCATCGCTCTCAGCTATGTCATCAACAATAATAGCTTAGGAGTAATATCAAGAGC 651
QY 243 TyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
Db 652 TTCAATCTTTCCGGGATGGGTGAGCGCGGCTGATCTCAGTTGATGATAGCCCGCGAC 711
QY 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
Db 712 TTGCTCCAGTATCAATCCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 771
QY 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
Db 772 AATTACTATCAAGGACGAGAGCCATGTTGTTACCCAAATGTTCTCTCCGATGGGT 831
QY 303 GlyAlaLalleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeu 322
Db 832 CGCGCAGCATACATGTCATAACCGCGCGTCTGACCGGTGCGAGCCCAATATCAAGCTT 891
QY 323 ValAsnValValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGln 342
Db 892 TCCACCTCGTCCGAGACACCGTGGCGTGACGACAGTCTTCTACTGTGTCTACGAA 951
QY 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
Db 952 CAGGAAGACAAAGAGGACGCTTGGCATCACTTGTCCAAAGATCTCATGGCCATCGCC 1011
QY 363 GlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGlu 382
Db 1012 GGTGAAGCCCTCAAGGCAAAATCACCACATAGGTGCTTGTGCTACCGCGGTGAGAA 1071
QY 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
Db 1072 CAACCTCTCTCTCAGCTCCCTAATCGGACGTAATAATCTTCAACCCGAAATGGAAACCA 1131
QY 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyArgAla 422
Db 1132 TACATACCGGATTTCAAGTGGCTTCGAACACATTTTGCATTACACGAGGACGAGCG 1191
QY 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 1192 GTGATCGACGACTCCAAAGAATCTACAACTATACAGGACACACGTTGAGGCTCAAGA 1251
QY 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
Db 1252 ATGACACTACATCGTTTGGTAACAGCTCATCTTCATCGTTATGTTACGAGCTTAGCTAC 1311
QY 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Db 1312 ATCGAGCTTAAAGGAGATAGGAGGCGATCGCGTTTGGCAAAATCGCGTTTGGGAGT 1371
QY 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluMet 502
Db 1372 GGTTCACAGTGAACCTCGCGGTGGAATGTAAACGTCAGATTAAAGACACACCTAAG- 1428
QY 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 1429 ---GAGCGACCATGGTCCGATTGTATCGACCGTACCCCTGTC 1467

```

RESULT 10

US-09-883-797-11

```

; Sequence 11, Application US/09883797
; Patent No. US20020066123A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemmiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES

```

```

; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/09/883,797
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 08/868,373
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-883-797-11

```

Alignment Scores:

```

Pred. No.: 1-82e-163 Length: 1502
Score: 1438.50 Matches: 279
Percent Similarity: 74.49% Conservative: 89
Best Local Similarity: 56.48% Mismatches: 113
Query Match: 53.68% Indels: 13
DB: Gaps: 6

```

US-09-883-797-2 (1-520) x US-09-883-797-11 (1-1502)

```

QY 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45
Db 25 ATGCACAGTCTCTAGCTCGGTGAAGCTCAAGTACGTGAACACTGGTTACCAATATTG 84
QY 46 CysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrValLeu 65
Db 85 GTTAAC-----CAATTCTTGAGTTTCTTTGATC---CCGATCATGGCTATTGTCGCC 135
QY 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85
Db 136 GTTGAGCTCTCTCGGATGGGCTGAAGAGATCCTTAATGTTTGAAT-----TCACATC 189
QY 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
Db 190 CAGTTTGACCTAGTTCAGGTTCTATGTTCTCTCTTTGTCATCTTCACTCCACCTGTT 249
QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
Db 250 TACTTCATGTCACAGCCAGCCACCATCTACCTCGTTGACTATCTTGTGTACAAGCCACCT 309
QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
Db 310 GTCACGCTGTCGTGTC-----CCCTGCGCACTTTCATGGAACACTCTCGTTGATC 360
QY 146 ThrAspAsp-----ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeu 162
Db 361 CTCAAGGACACAGCTTAAGAGCGTCGAGTTCGAATGAGAATCCTTGAACGTTCTGCGCTC 420
QY 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
Db 421 GGTGAGGAGACTGTCTCCCTCCGCTATTCATTATATTCCTCCCAACACCAACCATGGAC 480
QY 183 GluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
Db 481 CGCGCTAGAGCGAGGCTCAGATGGTTATCTTCGAGGCGCTAGGACCATCTTTTCAAGAAA 540
QY 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 541 ACCGGTCTTAAACCTTAAAGACGTCGACATCTTATCGTCAACTGCTCTCTTTCTCTCCC 600
QY 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
Db 601 ACACCATCGCTCTCAGCTATGCTATCAACAAATATAGCTTAGGAGTAAATATCAAGAGC 660
QY 243 TyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
Db 661 TTCAATCTTTCGGGATGGGTGACCGCGGCGCTGATCTCAGTTGATCTAGCCCGGAC 720
QY 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282

```


Db 721 TTGCTCCAGTTTCATCCCAATCAATCAATCATCGTCAGCAGGAGATCATAAGCGCT 780
Qy 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
Db 781 AATTAATCAAGGCAAGAGAGAGCCATGTTGTTTACCAATGTCTCTCCGCGATGGT 840
Qy 303 GlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeu 322
Db 841 CGCGCAGCCATACATGTCACACCGCGGTCTGACCGGTGGCGGCAAAATACAAGCTT 900
Qy 323 ValAsnValAlaArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGln 342
Db 901 TCCACCTCGTCGGGACACCGTGGCGTACGACCAAGTCTTCTACTGTGTCTACGAA 960
Qy 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
Db 961 CAGGAAGCAAAAGAGACAGTGGCATCACTTGTCCAAAGATCTCATGGCCATCGCC 1020
Qy 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyPrometValLeuProLeuSerGlu 382
Db 1021 GGTGAAGCCCTCAAGGCAAAATCACCACATAGTCTTGGTCTACCGCGTCAGAA 1080
Qy 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
Db 1081 CAATCTCTCTCCTCAGCTCCCTATCGGACGTAAATCTTCAACCCGAAATGGAACCA 1140
Qy 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAla 422
Db 1141 TACATACCGGATTTCAAGCTGGCTTCGAACACTTTTGATTCACGAGGAGGAGCGC 1200
Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 1201 GTGATCGACGAGCTCCAAAGAAATCTACAATCATCAGGAGAACACGTGAGGCGCTCAAGA 1260
Qy 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyr 462
Db 1261 ATGACACTACATCGTTTGGTAACACGTCATCTCATCGTATGTCAGGAGCTAGCTAC 1320
Qy 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Db 1321 ATCGAGCTCAAGGGAGAAATGAGGAGGAGCGATCGCGTTTGGGAAATCGCGTTGGGAGT 1380
Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
Db 1381 GGTTCCTCAAGTGAACCTCGCGTGTGGAAGTGAACCGTACGATTAAGACACCTAAG-- 1437
Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 1438 ---GACGGACCATGTCCTGATGATCGACCGTTACCTGTC 1476

RESULT 11

US-09-892-325-2
; Sequence 2, Application US/09892325
; Patent No. US20020116735A1
; GENERAL INFORMATION:
; APPLICANT: Kunst et al.
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme
; Involved In Very Long Chain Fatty Acid Synthesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell
; Leigh & Whinston, LLP
; STREET: One World Trade Center, Suite
; 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3.5-inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Word97 & ASCII

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,325
; FILING DATE: 26-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,947
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Earp, Ph.D.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 5493-50032/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1807
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-892-325-2

Alignment Scores:
Pred. No.: 2,47e-163 Length: 1807
Score: 1438.50 Matches: 279
Percent Similarity: 74.49% Conservative: 89
Best Local Similarity: 56.48% Mismatches: 113
Query Match: 53.68% Indels: 13
DB: 10 Gaps: 6

US-09-883-797-2 (1-520) x US-09-892-325-2 (1-1807)

Qy 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45
Db 74 ATGCCAGAGTTCTTCTAGTCGGTGAAGTCAAGTACGTGAACACTTGGTTACCAATATTG 133
Qy 46 CysAsnValThrThrIleLeuPheLeuIleLeuLeuProLeuThrGlyThrValLeu 65
Db 134 GTTAAAC-----CATTTCTTGAATTTCTTTTGTATC---CCGATCATGGTATTGTCGCC 184
Qy 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85
Db 185 GTTGAGCTTCTTCGGATGGTCTCTGAAGAGATCTTAATGTTTGGAAAT-----TCACTC 238
Qy 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
Db 239 CAGTTTGACCTAGTTTCAGGTTCTATGTTCTCTTCTTCTTGTCTATCTCATCTCCACTGTT 298
Qy 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
Db 299 TACTTCATGTCAGGCCAGCCACCATCTACCTCGTGTGACTATTTCTTTGTTACAGCCACCT 358
Qy 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
Db 359 GTCACGTGTCGTGTC-----CCCTTCGCAACTTTCATGGAACACTCTCGTTTGATC 409
Qy 146 ThrAspAsp-----ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeu 162
Db 410 CTCAGGACAAGCCCTAAGAGCGTCAGTTCCTCAAAATCAGAAATCTTGAACGTTCTGGCCCTC 469
Qy 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
Db 470 GGTGAGGAGACTTGTCTCCCTCCCGCTATTCATTATATTCCTCCACACCAACCATGGAC 529
Qy 183 GluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGlyLys 202
Db 530 GCGGCTAGAAGCGAGGCTCAGATGTTATCTTCGAGGCCATCGAGCATCTTTTCAAGAAA 589
Qy 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 590 ACCGGTCTTAAACCTAAAGACGTCGACATCTTATCGTCAACTGCTCTCTTTCTCTCC 649


```
Db 2363 GGTGAGGAGACTGTCTCCCTCGGCTATTCAATTATATCTCCACACCAACCATGGAC 2422
Qy 183 GluAlaArgAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
Db 2423 GCGGCTAGAGCGAGCTCAGATGTTATCTTCGAGGCCATGGACGATCTTTTCAAGAAA 2482
Qy 203 ThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
Db 2483 ACCGGTCTTAAACCTTAAAGACGTCGACATCTTATGCTCACTGCTCTCTTTCTCTCCC 2542
Qy 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleTysSer 242
Db 2543 ACACCATCGCTCTCAGCTAGTGTATCAACAATATAGCTTAGGAGTAATATCAAGAGC 2602
Qy 243 TyrAsnLeuGlyMetCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsn 262
Db 2603 TTCAATCTTTCCGGGATGGCTGCAGCGGGCCCTGATCTCAGTTGATCTAGCCCGCGAC 2662
Qy 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
Db 2663 TTGCTCAAGTTCATCCCAATTCAAATGCAATCATCTCGTCAGCAGCATCATACGCCT 2722
Qy 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
Db 2723 AATTACTATCAAGCAACGAGAGGCCATGTTGTACCAATTTGTCTCTTCGCGATGGCT 2782
Qy 303 GlyAlaAlaIleLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeu 322
Db 2783 GCGGCAGCCATACATGTCAAACCGCGGTCTACCGGTGGCGAGCCCAATACAAAGTT 2842
Qy 323 ValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnValTyrGln 342
Db 2843 TCCACCTCGTCCGGACACACCGTGGCGCTGACGACACAGTCTTCTACTGTGTCTACGAA 2902
Qy 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
Db 2903 CAGGAAGACAAAGAGGACACAGTGGCATCAACTGTGTCCTCAAGATCTCATGGCCATGCC 2962
Qy 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGlu 382
Db 2963 GGTGAAGCCCTCAAGGCAACATACACCAATAGTCTCTTGGTCTTACCGCGCTCAGAA 3022
Qy 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
Db 3023 CAACTTCTCTCTCAGTCCCTTAATCGGACGTAAATCTTCAACCCGGAATGGAACCA 3082
Qy 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAla 422
Db 3083 TACATACCGGATTCAAGCTGGCTTCGAACACTTTTGCACTTCCAGCAGGAGGAGAGCG 3142
Qy 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442
Db 3143 GTGATCGGACGCTCCAAAGAACTTACAACTATCAGGAGAACACGCTTGAAGCCTCAAGA 3202
Qy 443 MetThrLeuHisArgPheGlyAsnThrSerSerSerSerSerSerSerSerSerSerSer 462
Db 3203 ATGACATACATCGTTTGGTAACAGTCATCTTCATCGTTATGGTACGAGCTTACTAC 3262
Qy 463 ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer 482
Db 3263 ATCGAGTCTAAGGAGAGATGAGGAGCGGATCGGTTTGGCAATCGGTTGGGAGT 3322
Qy 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
Db 3323 GTTTCAGTGTAACTCTCGGCTGGGAAATGTAACCGTACGATTAAGACACCTAAG --- 3379
Qy 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 3380 ---GACGACCATGTCGATTTGATACGACCGTTACCTGTCTC 3418
RESULT 13
US-09-938-842A-2597
; Sequence 2597, Application US/09938842A
```

```
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2597
; LENGTH: 1653
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2597
```

Alignment Scores:

Pred. No.:	2,45e-163	Length:	1653
Score:	1438.00	Matches:	285
Percent Similarity:	68.77%	Conservative:	96
Best Local Similarity:	51.44%	Mismatches:	123
Query Match:	53.66%	Indels:	50
DB:	9	Gaps:	10

US-09-883-797-2 (1-520) x US-09-938-842A-2597 (1-1653)

```
Qy 2 AspArgGluArgLeuThrAlaGluMetAlaPheArg----- 13
Db 16 GAGCAAGATCTGCTCTCTACCGAGATCGTTAATCGTGGATCGAACCATCCGTCCTAAC 75
Qy 14 ---AspSerSerSerAlaValIleArgArgArgLeuProAspLeuLeuThrSer 32
Db 76 GCGCGCTCCCAACAGCTCTCGGTTAGGTCAGGTCAGGAGAGCTTGCTGATTTCTTCAGTCG 135
Qy 33 ValLysLeuLysTyrValLysLeuGlyLeuHisAsnSerCysAsnValThrIleLeu 52
Db 136 GTGAACCTGAAGTACGTGAACCTTGGTTACCACTACCTATAAACCATCGGTT----- 189
Qy 53 PhePheLeuIleLeuProLeuThrGlyThrValLeuValGlnLeuThrGlyLeuThr 72
Db 190 ---TATTTGGCGACCATACCG-----GTTCTGTGTGCTGGTTTATGTCGTGAG 234
Qy 73 PheAspThrPheSer-----GluLeuTrpSerAsnGlnAlaValGlnLeuAspThrAla 90
Db 235 GTTGGGAGTTTAAAGCAGAGAGAGATTTGG---AAGAAGCTTTGGGACATATGATCTGCA 291
Qy 91 ThrArgLeuThrCysLeuValPheLeuSerPheValLeuThr-----LeuTyrValAla 108
Db 292 ACTGTTATCGCA-----TTCTTCGCTGCTTTTAAACCGCTTGTGTCTACTTCATG 345
Qy 109 AsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGluAspGluArg 128
Db 346 TCTGCTCTCGCTCTCTTATCTTATTCGCTTGTTCACAGCCCTCCCATGAACAC 405
Qy 129 LysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPheThrAspAsp 148
Db 406 AAGTGACAAAAGAGAGATTCATAGCACTAGCGAAAAATCAGGAAGTTCAGCAAGAG 465
Qy 149 ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyValAspGluThrThrLeu 168
Db 466 ACATCGGTTTCAAGAAAGAGATCTTACAAGCCCTCAGCATAGGCCAGCAGACATACGTC 525
Qy 169 ProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAlaArgAlaGluAla 188
Db 526 CCAAGATCCATCTCTTCATCAAAAAACATAACACGATGAAAGAGGTCGTCAAGAGCC 585
```


Thu Feb 20 11:03:35 2003

us-09-883-797-2.p2n.rnpb

QY 276 SerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCys 295
Db 745 AGCAGAGAACATCCTTATACATTTACGCTGGTGATATAGTCCATGATGTTTCA 804
QY 296 AsnCysIlePheArgMetGlyGlyAlaIleLeuLeuSerAsnArgGlnAspArg 315
Db 805 RAATGCTTGTTCGCTGGTGGCGCGCTATTTCTCTCCAAACGCTGGAGATCGT 864
QY 316 LysLysSerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspLys 335
Db 865 AGACGGTCCAAAGTACGAGTAGTTACACGGTTCGACCGATACCGGAGCTGACGACAAG 924
QY 336 AsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAla 355
Db 925 TCTTTTCGTTGCGTGCAACAAGGAGAGCGATGAGAACGCAAAATCGGAGTGAGTTGTCC 984
QY 356 ArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyPro 375
Db 985 AAGGACATAACCCGATGTTGCTGTCGAACGGTTAAGAAACACATAGCAACGTTGGGTCCG 1044
QY 376 MetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMet 395
Db 1045 TTGATTCCTCCGTTAGCGAGAACTCTTTTTCGTTACCTTCATGGGCAAGAACTT 1104
QY 396 PheLysLeuLysValLysPro---TyrIleProAspPheLysLeuAlaPheGluHisPhe 414
Db 1105 TTCAAGATAAAATCAAAACATTACTAGCTCCGGATTTCAAACTTGCTATTGACCAITTT 1164
QY 415 CysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLys 434
Db 1165 TGTATACATCCGGAGGAGAGCCGCTGATGTGCTAGAGAGAACCTAGCCCTAGCA 1224
QY 435 AspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSer 454
Db 1225 CCGATCGATGTAGAGGCATCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGC 1284
QY 455 SerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArg 474
Db 1285 TCAATATGGTATGATGGCATACATAGAACCAAAAGGAGGATGAAGAAAGTAATAAA 1344
QY 475 LeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeu 494
Db 1345 GTTTGGCAGATGCTTTAGGCTCAGGCTTAAAGTCTAACAGTCCAGTTTGGGTGGCTCTA 1404
QY 495 ArgProValSerThrGluGluMetThrGlyAsnAlaTyrAlaGlySerIleAspGlnTyr 514
Db 1405 AACATGTCAAAGCTTCG-----ACAAATAGTCTCTGGGAACACTGCATCGACAGATAC 1458
QY 515 ProValLysVal 518
Db 1459 CCGGTCAAATTT 1470

Search completed: February 19, 2003, 11:45:30
Job time : 160 secs


```
Db 271 ATCATCTGTTACGCGATTCTAGTCTTCGGGTTAAAGGTTTATGTTATGATACCCGACCTAGA 330
QY 113 ProValTyrLeuValAspPheSerCysTyrLysProGluAspGluArgLysIleSerVal 132
Db 331 CCGGTTTACTGTTGTTGTTCTCTGTTATCTCCACCTGATCATCTCAAAGCTCCCTTAC 390
QY 133 AspSerPheLeuThrMetThrGluGluAsnGlySerPheThrAspPheThrValGlnPhe 152
Db 391 GCTCGGTTTCATGAACATCTTAGACTACCGGAGATTTCGATGACTCTGCTCTCGAGTTT 450
QY 153 GlnGlnArgIleSerAsnArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIle 172
Db 451 CAACGCAAGATCTCTGAGCTTCTGTTGTTAGGGAACACACTTATGCTCCCTGAAGCTATG 510
QY 173 ThrSerThrProProLysLeuAsnMetSerGluAlaArgAlaGluAlaGluAlaValMet 192
Db 511 CATTATGTTCCACCGGAGATTCTCAATGGCTGCTAGAGAAGAGCTGAACAGTCAATG 570
QY 193 PheGlyAlaLeuAspSerLeuPheGluLysThrGlyIleLysProAlaGluValGlyIle 212
Db 571 TTTGGTCTTTAGATAACCTTTTCGCTAACACTTAATGTAACCAAGGATATGGATC 630
QY 213 LeuIleValAsnCyssSerLeuPheAsnProThrProSerLeuSerAlaMetIleValAsn 232
Db 631 CTGTGTGTAATGTAGTCTCTTAATCAACTCTCTGTTATCTGCAATGATGTGAAC 690
QY 233 HisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGlyMetGlyCysSerAla 252
Db 691 AAGTATAGCTTAGAGTAACATTAAGAGCTACAATCTAGGCGGTATGGGTTGCAGCGCG 750
QY 253 GlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAla 272
Db 751 GGAGTTATCGCTGTGATCTTCTAAAGACATGTTGTTGTATAGTACATAGGACACTTATCG 810
QY 273 ValValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMet 292
Db 811 GTTGTGTTCTTCTAGAGAACATTAATCTAGAAATGGTATTTGGTAAACAAGAAATCGATG 870
QY 293 LeuLeuCysAsnCyssIlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgAlq 312
Db 871 TTGATACCGAAGCTGTTGTTTCGAGTTGGTGCTCTGCGGTTTGTCTATCGAACAGTCG 930
QY 313 GlnAspArgLysLysSerLysTyrSerLeuValAsnValValArgThrHisLysGlySer 332
Db 931 AGGCACAGACGGCTTAAGTACAGGCTTGATACATGTAGTACGAGCTCACCGTGGAGCA 990
QY 333 AspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyVal 352
Db 991 GATGATAAAGCTTTCCGTTGTTTATCAAGAGCAGGATGATACAGGAGAACCGGGTT 1050
QY 353 SerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThr 372
Db 1051 TCGTTGTGGAAGATCTAATCGGATTCAGGGAACTCTCAAAACCAATATCACTACA 1110
QY 373 LeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLys 392
Db 1111 TTGGTCTCTGTTCTTACCGATAGTGAGGAGATCTCTCTTTTACTGACTCTAGTTG 1170
QY 393 ArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLysLeuAlaPheGlu 412
Db 1171 AAGAAGCTCTTAAACGGTAAAGTGAACCGTATATCCCGGATTTCAAACTGCTTTCGAG 1230
QY 413 HisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAsp 432
Db 1231 CATTTCTGTATCCATGCTGGTGAAGAGCTGTGATCGATGATGAGTGAAGAAGAAATCTGCAG 1290
QY 433 LeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSer 452
Db 1291 CTTTACCAGTTCATGCTGAGGCTTCGAGGATGACTCTTCACTGATTTGGTAACACATCT 1350
QY 453 SerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGly 472
Db 1351 TCGAGCTCCATTTGGTATGAATGGCTTACATTCAAGCAAGGAGGAGATCGCAGAGAGT 1410
```

```
QY 473 AspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLys 492
Db 1411 AATCGGTTTGGCAATCGGTTCCGAAGTGGATTTAAATGTATATAGCGGATTTGGAA 1470
QY 493 AlaLeuArgProValSerThrThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAsp 512
Db 1471 GCATTAAAGCATGTG-----AAACCTTCGACAACAGCTCTTGGGAAGATTGTTATTGAC 1524
QY 513 GlnTyrProVal 516
Db 1525 AAGTATCCGTA 1536
RESULT 3
US-08-868-373-9
; Sequence 9, Application US/08868373
; Patent No. 6307128
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Post-Beittemiller, Martha A.
; APPLICANT: Todd, James
; TITLE OF INVENTION: FATTY ACID ELONGASES
; FILE REFERENCE: 07148/064001
; CURRENT APPLICATION NUMBER: US/08/868,373
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-868-373-9
Alignment Scores:
Pred. No.: 3,76e-174 Length: 1611
Score: 1531.50 Matches: 285
Percent Similarity: 76.20% Conservative: 96
Best Local Similarity: 57.00% Mismatches: 104
Query Match: 57.15% Indels: 15
DB: 4 Gaps: 4
US-09-883-797-2 (1-520) x US-08-868-373-9 (1-1611)
QY 23 ArgArgArgLeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeu 42
Db 139 AGAGAAAGCTTCCTAATTTCTTACAAAGCGTCAACATCAATACGTCAAGTAGGTTAT 198
QY 43 HisAsnSerCysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGly 62
Db 199 CAT-----TACCTCATTTACTCATCTCTTCAAGCTCTGTTGGTCCATTATGGCG 249
QY 63 ThrValLeuValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsn 82
Db 250 GTTTTATGTCACAGAGATCTCTCGATTAAACAACAGACGATCTTTACAGATTGG----- 303
QY 83 GlnAlaValGlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSer----- 100
Db 304 -----CTTCATCTCCAATACTCTGCTGCTTCATCTCTCTCTCTCTCTCTCTCTTA 351
QY 101 -----PheValLeuThrLeuTyrValAlaAsnArgSerLysProValTyrLeuValAsp 118
Db 352 GCTATCTTTGGCTCCACCGTTTACATCATGATGATGCTCCAGATCTGTTTATCTGCTTAT 411
QY 119 PheSerCysTyrLysProGluAspGluArgLysIleSerValAspSerPheLeuThrMet 138
Db 412 TACTCTTTGTTATCTCTCCGAGAGTCTTCAGGTTAAGTATCAGAAAGTTTATGGATCAT 471
QY 139 ThrGluGluAsnGlySerPheThrAspThrValGlnPheGlnArgIleSerAsn 158
Db 472 TCTAAGTTGATCAAGATTCAATGATGATGATCTTACAGTTTACAGAGAAAGATCTCTGAA 531
QY 159 ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLys 178
Db 159 ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProLys 178
```


US-08-265-047-3

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

1,24e-172

1519.50

75.30%

57.49%

56.70%

1

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

1783

284

88

115

7

4

US-09-883-797-2 (1-520) x US-08-265-047-3 (1-1783)

QY

26

LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer

45

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||

DB	970	GTAGCCACCCACAGGGCGCTGACGACAGTCTTATAGATGGCTTACACACAGAGAT	1029
QY	346	GluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAla	365
DB	1030	GAATAAACAAGGTAGTGTTCCTTATCCAAAGGATCTGATGGCAGTTCGCCGTGAAGCC	1089
QY	366	LeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMet	385
DB	1090	CTAAAGGCCAACATCACGACCCCTTGGTCCCTCTGCTCCCATGTTCAGAACACCTCTC	1149
QY	386	PheLeuIleSerLeuValLysArgLysMetPheLysLeu---LysValLysProTyrIle	404
DB	1150	TTCITTCACCTAGTGGCACCTAAGGTCTTCAAGATGACGAACCTGAAGCCATACATC	1209
QY	405	ProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeu	424
DB	1210	CCAGATTCAAGTTGGCAGCGAAGCATTCTGCATCCATCAGGAGGCAAGCAGTGTG	1269
QY	425	AspGluValGlnLysAsnLeuAspLysAspTyrPheHisMetGluProSerArgMetThr	444
DB	1270	GATGAGCTCGAGACCACTTGGAGTTGACGCCATGGCACCTTGAACCTCGAGGATGACA	1329
QY	445	LeuHisArgPheGlyAsnThrSerSerSerSerSerSerSerSerSerSerSerSer	464
DB	1330	CTGTATAGGTTTGGGAACACATCGAGTAGCTCATTTATGGTACGATTTGGCATACGCTGAA	1389
QY	465	AlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGlyPhe	484
DB	1390	GCNAAAGGAGGATCCGTAAGGATGATCGAATTTGGATTTGGTTTGGTTCAGGTTTC	1449
QY	485	LysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThrGly	504
DB	1450	AAGTCTAACAGTGTGTGTGGAGGCTTTGAGGAGTGTCAATCCGCGCTAGA---GAGAAG	1506
QY	505	AsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal	518
DB	1507	AATCCTTGGATGATGAAATTGAGATTTCCTTCTCCATGTG	1548

RESULT 6
US-08-066-299-10
Sequence 10, Application US/08066299
Patent No. 5445947
GENERAL INFORMATION:
APPLICANT: James George Metz
APPLICANT: Kathryn Dennis Lardizabal
APPLICANT: Michael W. Lassner
TITLE OF INVENTION: Fatty Acyl CoA: Fatty Alcohol
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066,299
FILING DATE: 19930520
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOVEMBER-1991
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUGUST-1992
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOVEMBER-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 REFERENCE/DOCKET NUMBER: CGNE 98
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1733 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-066-299-10

Alignment Scores:
 Pred. No.: 6,05e-170 Length: 1733
 Score: 1497.00 Matches: 282
 Percent Similarity: 74.75% Conservatives: 88
 Best Local Similarity: 56.97% Mismatches: 117
 Query Match: 55.86% Indels: 8
 DB: 1 Gaps: 5

US-09-883-797-2 (1-520) x US-08-066-299-10 (1-1733)

QY 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuLysGlyLeuHisAsnSer 45
 Db 120 CTCGCCCACTTCAAGTCTCCATCAACTTACACACGCTCAAGCTCGGCTACCAAC----- 173
 QY 46 CysAsnValThrIleLeuPhePheLeuIleLeuLeuProLeuThrGlyThrValLeu 65
 Db 174 ---TACTTAATCTCAATGCCCTCTCTCTCGTATTCATCCCCCTTTTGGGCTCGCTCGC 230
 QY 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuLeuTrpSerAsnGlnAlaVal 85
 Db 231 GCCCATCTCTCTCTCGGCCCATGACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 284
 QY 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
 Db 285 CGCGCAACCT 344
 QY 106 TyrValAlaAsnArgSerLysProValLysLeuValAspPheSerCysTyrLysProGlu 125
 Db 345 CATTTCTTGACCGCGCCAGGAATGCTACTTGTGTGACTTGTGATGCTATAAGCCCTCAA 404
 QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
 Db 405 CCGAACCCTGATGACATCCACAGAGATGTTTCATGGACCGGACCTCCCGCGCGGCTCGTTT 464
 QY 146 ThrAspAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAspGlu 165
 Db 465 TCTAAGGAGAAATATTGAGTTTCAGAGGAAGATCTTGAGAGGCGCGGTATGGGTGGGAA 524
 QY 166 ThrTyrLeuProArgGlyIleThrSerThrProLysLeuAsnMetSerGluAlaArg 185
 Db 525 ACCTATGTCGCCGAATCCGTCACAAAGGTGCGCGCGGACGATGATGACGAGCGCCAGG 584
 QY 186 AlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyLe 205
 Db 585 GCGGAGCGGAGAGGTGATGATCGGGGGGATCGAGGTGTTGGAGAGACGCGGGGTG 644
 QY 206 LysProAlaGluValGlyIleLeuIleValAsnCysSerLeuPheAsnProThrProSer 225
 Db 645 AAGCCGAGCAGATAGGAATAGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 704
 QY 226 LeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeu 245
 Db 705 CTGTCATCATGATAGTTAAACCATACAAAGCTNAGGGGTAATATATCTAGCTATAATCTT 764
 QY 246 GlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLeuLys 265

Db 765 GGTGCATGGGTTCAGTCTGGGCTCATTTCCATTGATCTTGCACAGACCTCCCTACAG 824
 QY 266 Ala---AsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrp 284
 Db 825 GTTTACCGTAAACACATATGTGTAGTAGTGAGCAGCAGAAACATGACCCCTTAATGG 884
 QY 285 TyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAla 304
 Db 885 TACTGGGCAATGACCGCTCCATGCTATCACCACCTGCCTATTTCCGATGGGTGGGCT 944
 QY 305 AlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuValAsn 324
 Db 945 GCCATATCTCTCAACCGCTGGGCTGATCTGCGCGGATCAAGTACCACTCCCTCAT 1004
 QY 325 ValValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLysGlu 344
 Db 1005 ACAGTAGCCACCCCAAGGCGCTGACGACAGTCTTATAGATGCTCTTACAACAAGAA 1064
 QY 345 AspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAsp 364
 Db 1065 GATGAAATAACAAGGTAGGTGTTCCCTTATCCCAAGGATCTGATGGCAGTTCCCGGTAA 1124
 QY 365 AlaLeuLysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGluGlnLeu 384
 Db 1125 GCCCTAAAGGCCAACATCAGCACCTTGGTCCCTCGTCTCCCATGTGACAAACATC 1184
 QY 385 MetPheLeuIleSerLeuValLysArgLysMetPheLysLeu---LysValLysProTyr 403
 Db 1185 CTCTTCTTCCACCTTAGTGGCAGTAAGGTCTTCAAGATGACGACAGCTGAAGCCATAC 1244
 QY 404 IleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaVal 423
 Db 1245 ATCCCAAGATTCAAGTTGGCAGCAGACACTTCTGTCATCCATGACGAGGAGCAACAGTG 1304
 QY 424 LeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMet 443
 Db 1305 TTGGATGAGCTCAGAGAAGAACTTGGAGTTGACGCCATGGCCACTTGAACCTCGAGGATG 1364
 QY 444 ThrLeuHisArgPheGlyAsnThrSerSerSerSerSerSerSerSerSerSerSerSer 463
 Db 1365 ACACCTATAGGTTTGGGAACACATCGAGTAGCTCATTTATGTTAGGATGGCATAACCT 1424
 QY 464 GluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGly 483
 Db 1425 GAAGCAAAAGGGAGGATCCCTAAAGGTGATCGAACTTGGATGATTTGGTTTCAGGT 1484
 QY 484 PheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMetThr 503
 Db 1485 TTCAAGTGTAAACAGTCTTGTGTGGAGGGCTTTGAGGAGTGTCAATCCGGCTAGA---GAG 1541
 QY 504 GlyAsnAlaTrpAlaGlySerIleAspGlnTyrProValLysVal 518
 Db 1542 AAGAATCTCTGGATGGATGAAATTGAGAAGTTCCCTCTCCATGTG 1586

RESULT 7

US-08-265-047-2
 ; Sequence 2, Application US/08265047
 ; Patent No. 5679881
 ; GENERAL INFORMATION:
 ; APPLICANT: Metz, James G.
 ; APPLICANT: Lardizabal, Kathryn D.
 ; APPLICANT: Lassner, Michael
 ; TITLE OF INVENTION: Nucleic Acid Sequences Encoding a Plant Cytoplasmic Protein
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Calgene, Inc.
 ; STREET: 1920 Fifth Street
 ; CITY: Davis
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 95616
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,047
FILING DATE: 23-JUN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/160,602
FILING DATE: 30-NOV-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/796,256
FILING DATE: 20-NOV-91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/933,411
FILING DATE: 21-AUG-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,299
FILING DATE: 20-MAY-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09863
FILING DATE: 13-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2 :
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
IS-08-265-047-2

Alignment Scores:		
Pred. No.:	6, 05e-170	1733
Score:	1497.00	282
Percent Similarity:	74.75%	Conservative: 98
Best Local Similarity:	56.97%	Mismatches: 117
Query Match:	55.86%	Indels: 8
DB:	1	Gaps: 5

US-09-883-797-2 (1-520) x US-08-265-047-2 (1-1733)

Qy	26	LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer	45
Db	120	CTCCCGAACTTCAGTCTCATCAACTTACACACAGCTCAAGCTCGGTACCAC	173
Qy	46	CysAsnValThrIleLeuPhePheLeuIleIleLeuProLeuThrGlyThrValLeu	65
Db	174	--TACTTTAATCTCCAATGCCTCTCTCCTGATTATCATCCCCCTTTGGGCTCGCTCG	230
Qy	66	ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal	85
Db	231	GCCCATCTCTCCTCTCTCGGCCCATGACATGTGTCCTCTCTCTC-----GACCTCTCCT	284
Qy	86	GlnLeuaspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu	105
Db	285	CGCGCAACCTCCCTCCCTGTTGTTGTTCTCTTCCTCTTCGTTTTATTAGCAACCTTA	344
Qy	106	TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCystYrLysProGlu	125
Db	345	CATTCTTGACCGCCCGCAGAATGCTACTGTGGTGGACTTTGGATGCTATAAGCCTCAA	404
Qy	1185	CTCTCTTTGGCCACCTTAGTGGCAGTAAAGGTCTTCAAGATGACGAACGTGAAGCAVAC	1244
Qy	404	IleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyIcLYargAlaVal	423
Db	1245	ATCCCAGATTTCAGTTGGCAGCGAACGACTTCTGCATCCATGCGAGGAGCAAGCAGTG	1304
Qy	424	LeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMet	443
Db	1305	TGGATGAGCTCGACAAGAACATTGGAGTTGACGCCATGGCACTTGAACCCCTCGAGGATG	1364
Qy	444	ThrLeuHisArgPheGlyAsnThrSerSerSerLeuTrpTyrcylumMetalatyrThr	463
Db	1365	ACACTGTATAGTGTGGGAACACATCGAGTAGCTCATATTATGTACAGTGGCATACGCT	1424
Qy	464	GluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGly	483
Db	1425	GAAGCAAAAGGGAGGATCCGTAAGGTTGATCGAACTTGGATGATTGGATTGGTTCCAGGT	1484

QY 483 GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet 502
 Db 1381 GGTTCAGTGAATCTCGCGTGGAGTGTAAACGTCAGCATTAAGACACACCTAAG--- 1437
 QY 503 ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
 Db 1438 ---GACGGACCATGGTCCGATGTATCGACCGTTACCTGTC 1476

RESULT 12

US-09-058-947A-2

; Sequence 2, Application US/09058947A

; Patent No. 6274790

; GENERAL INFORMATION:

; APPLICANT: Kunst et al.

; TITLE OF INVENTION: Nucleic Acids Encoding Plant Enzyme

; TITLE OF INVENTION: Involved In Very Long Chain Fatty Acid Synthesis

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell

; ADDRESSEE: Leigh & Whinston, LLP

; STREET: One World Trade Center, Suite

; CITY: Portland

; STATE: OR

; COUNTRY: USA

; ZIP: 97204-2988

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3.5-inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows NT

; SOFTWARE: Word97 & ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/058,947A

; FILING DATE:

; CLASSIFICATION: 800

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 60/043,831

; FILING DATE: April 14, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: David J. Earp, Ph.D.

; REGISTRATION NUMBER: 41,401

; REFERENCE/DOCKET NUMBER: 5493-50032/DJE

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1807

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-09-058-947A-2

Alignment Scores:

Pred. No.:

Score: 7.14e-163

Percent Similarity: 1438.50

Best Local Similarity: 74.49%

Query Match: 56.48%

Db: 53.68%

Length: 1807

Matches: 279

Conservative: 89

Mismatches: 113

Indels: 13

Gaps: 6

US-09-883-797-2 (1-520) x US-09-058-947A-2 (1-1807)

QY 26 LeuProAspLeuLeuThrSerValLysLeuLysTyrValLysLeuGlyLeuHisAsnSer 45

Db 74 ATGCCAGAGTCTCTAGTTCGGTGAAGCTCAAGTACGTGAACACTTGGTTACCAATATTG 133

QY 46 CysAsnValThrIleLeuPhePheLeuIleLeuProLeuThrGlyThrValLeu 65

Db 134 GTTAAC-----CATTTCCTGAGTTTCTTTTGATC---CCGATCATGCTATTGTGCGC 184

QY 66 ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal 85

Db 185 GTTAGCTTCTTCGATGGGTCCTGAAGAGATCCCTAATAGTTTGAAT-----TCACATC 238
 QY 86 GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu 105
 Db 239 CAGTTTGACCTAGTTCAGGTTCTATGTTCTTCCCTTCTTGTTCATCTTCACTCCACTGTT 298
 QY 106 TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu 125
 Db 299 TACTTCATGTCCAAAGCCAGCACCATCTACCTGTTGACTATTCTTGTGTACAGCCACCT 358
 QY 126 AspGluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPhe 145
 Db 359 GTCACGTGTCGTGTC-----CCCTTCGCAACTTTCATGGAACACTCTCGTTTGTATC 409
 QY 146 ThrAspAsp-----ThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeu 162
 Db 410 CTCAAGGACCAAGCCTAAGAGCGTGCAGATGGTTATCTTCGAGGCCATGGACGATCTTTC 469
 QY 163 GlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLysLeuAsnMetSer 182
 Db 470 GGTGAGGAGACTTGTCTCCCTCCGCTATTCAATTATTCCTCCACACCAACCATGGAC 529
 QY 183 GluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLys 202
 Db 530 GCGGCTAGAGCGAGGCTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTCACAGAA 589
 QY 203 ThrGlyLeuLysProAlaValGlyIleLeuIleValAsnCysSerLeuPheAsnPro 222
 Db 590 ACCGGTCTTAACCTAAGACGTCGACATCCTTATCGTCAACTCTCTCTCTTCTCTGCC 649
 QY 223 ThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSer 242
 Db 650 ACACCATCGCTCTCAGCTATGGTCATCAACAAATATAAGCTTAGGAGTATATCAAGAGC 709
 QY 243 TyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIleSerLeuAspLeuAlaAsnAsn 262
 Db 710 TTCATCTTTCGGGATGGGCTGACGCGGGCTCATCTCAGTTGATCTAGCCCGGAC 769
 QY 263 LeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeu 282
 Db 770 TTGCTCCAAGTTCATCCCAATCAATGCAATCATCGTCAGCAGGAGATCAACCCCT 829
 QY 283 AsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGly 302
 Db 830 AATTACTATCAAGGCAAGGAGAGCCATGTTGTTACCCAAATGTTCTCTTCCGATGGGT 889
 QY 303 GlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeu 322
 Db 890 CGCGCAGCCATACATGTCAAACCGCCGCTGACCGGTGCGGAGCCCAATACAGCTT 949
 QY 323 ValAsnValValArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGln 342
 Db 950 TCCACCTCGTCGGGACACACCGTGGGCTGACGACAACTCTTCTTCTACTGTGTACGAA 1009
 QY 343 LysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAla 362
 Db 1010 CAGGAACAAAGAGGACAGCTTGGCATCAACTTGTCCAAAGATCTCATGCCATCGCC 1069
 QY 363 GlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGlu 382
 Db 1070 GGTGAAGCCCTCAAGGCAAAACATCACCACATAGTCTTGTCTCTCCCGGCGTCAGAA 1129
 QY 383 GlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysPro 402
 Db 1130 CACTTCTCTCTCCCTCAGTCCCTAATCGAGGATTAATCTTCAACCCGAAATGGAACCA 1189
 QY 403 TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyClyArgAla 422
 Db 1190 TACATACCGGATTCAGCTGGCCCTTCGACACTTTTGCATTCACGAGGAGGACGAGCG 1249
 QY 423 ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg 442

Db	3023	CAACCTTCTCTCTCCTCAGTCGCCCTAATCGGACGCTAAATCTTCAACCCGAAATGGAACCA	3082
QY	403	TyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyArgAla	422
Db	3083	TACATACCGGATTTCAAAGCTGCCCTCGAACACTTTTGCTATTCACGAGGCGACGCG	3142
QY	423	ValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArg	442
Db	3143	GTGATCGCAGAGCTCCAAAGAAGATCTACACATATCAGGAGAACACCGTTGAGGCCTCAAGA	3202
QY	443	MetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTrpGluMetAlaTyr	462
Db	3203	ATGACACTACATCGTTTGGTAACACGTCATCTTCATCGTTATGTACGAGCTTAGCTAC	3262
QY	463	ThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAlaPheGlySer	482
Db	3263	ATCGAGTCTAAAGGAGAGAAATGAGGAGAGCGCATCGGTTTGGCAAATCGGTTGGGAGT	3322
QY	483	GlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThrGluGluMet	502
Db	3323	GGTTTCAAGTGTAACCTCTGCCGTGTGGAAATGCTAACCGGTACCATTAAGACACCTAAG---	3379
QY	503	ThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal	516
Db	3380	---GACGGACCATGGTCGATGTGATCAGCGTTACCGTGTC	3418

Qy	127	GluArgTysIleSerValAspSerPheLeu-----ThrMetThrGluGluAsnGly	141
Db	313	CATCTCAAGGTCAGTATCCAAACCTAATGGACACACGCAAGACGTCGAAGACGACGC	372
Qy	144	-----SerPheThrAspThrValGlnPheGlnAlaGilesSerAsn	158
Db	373	ATGTGTTGGAGAACAAGAGAGCGGACCATTTAGTTGACTTCCAGAGAAAGATTCTTGA	432
Qy	159	ArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThrProProLys	178
Db	433	CGTTCGGGCTCTGTGTCAAAGAAACCTACATCCCGAGGCTCTCAGTGCCTCCACTTTC	492
Qy	179	LeuAsnMetSerGluAlaArgAlaGluAlaGluAlaValMetPheGlyAlaLeuAspSer	198
Db	493	CAAGGCATGGTGCTCCAGCTAAAGAGACGGAAGAAGTAATCTTCGGAGCTCTTCACAA	552
Qy	199	LeuPheGluLysThrGlyIleLysProAlaGluValGlyIleLeuIleValAsnCyssSer	218
Db	553	CTTTTTCGCAACACCGGTGTAACCTCGATCATATCGGTATATTGGTGGTGAATTCAG	612
Qy	219	LeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGlu	238
Db	613	ACGTTTAATCCAACTCCATCCTCGCTCCCATGATTGTGAACAAGTACAAACTCAGAC	672
Qy	239	AspIleLysSerTyrAsnLeuGlyGlyMetGlyCyssSerAlaGlyLeuIleSerIleAsp	258
Db	673	AACATCAAGAGTTGAATCTTGGAGGATGGTTCAGTGCAGGAGTTATAGCTGTGTTGAT	732
Qy	259	LeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGlu	278
Db	733	GTCCCTCAAGGGATTACTACAAGTTCTATAGAAACACTTATGCTATTAGTAAGCACAG	792
Qy	279	AsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIle	298
Db	793	AACATCCTCAGAACTATACTTGGGAAACAAATCAATGCTAGTACAAACTGTTTG	852
Qy	299	PheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgLysLysSer	318
Db	853	TTCCGGCTGGTGCTGCGGTCTGCTTCAACACAGATCTAGACACGCTAACCGCGCC	912
Qy	319	LysTyrSerLeuValAsnValValArgThrHisLysClySerAspLysAsnTyrAsn	338
Db	913	AAATACGAGCTGTTACACCCGTACCGATCCATACCGGATCAGATGATAGTGGTTCGA	972
Qy	339	CysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeu	358
Db	973	TGTGCACACAAGAGAGGATGAAGATGGTATTAATGGAGCTTACCTTGACAAGAACTA	1032
Qy	359	MetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeu	378
Db	1033	CCTATGGTGGCTGCAAGGACTCTTAAGATAAATATCCCACTTTGGTCTCTCTGTACTT	1092
Qy	379	ProLeuSerGlnGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeu	398
Db	1093	CCATTAAAGAGAAGCTACCTCTCTTATTACTTTTGTCAAGAGAAGTATTTCACGCCA	1152
Qy	399	LysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHisAla	418
Db	1153	GAGTTAAAGAAATATACACCATTTCAAGCTTGCCCTTTGAGCATTTCTGTATCCACGCT	1212
Qy	419	GlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMet	438
Db	1213	GGTGAAGAGCTCTAATAGATGAGCTGGAGAGAACCCTTAAGCTTTCCTCGTTACAGTA	1272
Qy	439	GluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerLeuLeuTrpTyr	458
Db	1273	GAGCGCTCAAGAATGACACTCACAGGTTTGTTAACTTCTCTAGCTCAATCTCGTAC	1332
Qy	459	GluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIle	478
Db	1333	CAGTTAGCTTATACAGAAGCTTAAGGAAGGATTGAAGAGAGATAGGATTGGCAGATT	1392
Qy	479	AlaPheGlySerGlyPheLysCyssAsnSerAlaValTrpLysAlaLeuArgTrpValSer	498

D	61	TGT-----	-----TTGTTCCGGTTTAACGGCGTGTCTCTCGCC	90
Q	66	ValGlnLeuThrGlyLeuThrPheAspThrPheSerGluLeuTrpSerAsnGlnAlaVal	85	
D	91	GGAAAGGCTCTCGGCTTACCATAAAGCATCTCCACAACTCTCTTCTCTATCTCCAAAC	150	
Q	86	GlnLeuAspThrAlaThrArgLeuThrCysLeuValPheLeuSerPheValLeuThrLeu	105	
D	151	AACCTTATACAGTAACTTTACTC-----TTTGCTTTCACGTGTTTTCGGTTTGGTCTC	204	
Q	106	TyrValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGlu	125	
D	205	TACATCGTAACCGCCCAATCGGTTTATCTCGTTGTACTACTCGTTGTACCTTCCACCA	264	
Q	126	AspGluArgLysIleSerValAspSerPheLeuThrMet-----	138	
D	265	CGCATCTCAAAGTTAGTGTCCTAAAGTCAATGGATATTTTCTACCAATAAGAAAAGCT	324	
Q	139	---ThrGluAsnGlySerPheThrAspAsp-----ThrValGlnPheGlnGlnArg	155	
D	325	GATACTCTTCACGGAACGTGGCATGTGATGATCGTCTCGCTCGATTTCTCTGAGGAAG	384	
Q	156	IleSerAsnArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIleThrSerThr	175	
D	385	ATTCAAGAGCGTTCAAGTCTAGGTGATGAGAGCTACAGTCTTGAGGAGCTCATTCAGTA	444	
Q	176	ProProLysLeuAsnMetSerGluAlaAlaArgAlaGluAlaValMetPheGlyAla	195	
D	445	CCACCGGGAGACTTTTGCAGCGTCACGTGAAGACAGACAGAGGTATATCATCGGTGCG	504	
Q	196	LeuAspSerLeuPheGluLysThrGlyLysProAlaGluValGlyIleLeuIleVal	215	
D	505	CTCGAAATCTATTTCGAGAACCAACCAAGTTTACCCTAGAGAGATGGTATACITGTGGTG	564	
Q	216	AsnCysSerLeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLys	235	
D	565	AATCAAGCAATGTTTATCCAACTCTTCGCTATCGCTATCGCTATGCTCGTAACTTTCAAAG	624	
Q	236	MetArgGluAspIleLysSerTyrAsnLeuGlyMetGlyCysSerAlaGlyLeuIle	255	
D	625	CTCCGAAGTAACATCAAAAGCTTTAATCTAGGAGGAATGGTGTAGTGTGGTGTATT	684	
Q	256	SerIleAspLeuAlaAsnAsnLeuLeuLysAlaAsnProAsnSerTyrAlaValValVal	275	
D	685	GCCATTGATTGGTTAAAGACTTGTTCATGTTTCATATAAACACTTATGCTCTTGTGGTG	744	
Q	276	SerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCys	295	
D	745	AGACTGAGACATCACACAGGCATTTATGCTGGAGAAATAGATCAATGATGGTTAGC	804	
Q	296	AsnCysIlePheArgMetGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArg	315	
D	805	AATTGCTTGTTCGTGTTGGTGGGCGCGATTTCGTCCTAACAGTCGGGAGACCGG	864	
Q	316	LysLysSerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspLys	335	
D	865	AGACGGTCCAAGTACAGCTAGTTACACGGTCCGACGCATCTGAGGAGCTGATGACAAG	924	
Q	336	AsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAla	355	
D	925	TCCTTTCGATGTGTCAACAAGAAGACGATGAGAGCGCGCAAAATCGGAGTTTGTCTGCA	984	
Q	356	ArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyPro	375	
D	985	AAGGACATTAACCAATGTTCCGGGGACACACTATACGAAAAATATAGCAACATTTGGTCCG	1044	
Q	376	MetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMet	395	
D	1045	TTGATCTCTCTTTAAGCGAAAAGTTCTTTTTCGCTACCTTCGTCGCCAAGAACAAT	1104	
Q	396	PheLysLeuValLysPro---TyrIleProAspPheLysLeuAlaPheGluHisPhe	414	
D	1105	CTAAAGGATAAAATCAAGCATTAATATGTTTCGGGATTTCAAGCTTGCCTGACCATTTTC	1164	

QY 415 CysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLys 434
Db |||||||
1165 TGTATTTCATGCGGAGGAGCCGTCGATCGTAGCTAGAGAAGAACTTAGGACTATCG 1224
QY 435 AspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSer 454
Db |||||||
1225 CCGATCGATGTGGAGGCATCTAGATCAACGTTACATAGATTTGGGAATACTTCATCTAGC 1284
QY 455 SerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArg 474
Db |||||||
1285 TCAATTGGTATGAATTAGCATACATAGAGGCAAGGCAAGCAATGAAGAAAGGAATAAA 1344
QY 475 LeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeu 494
Db |||||||
1345 GCTTGGCAGATTGCTTTAGGATCAGGTTTAAGTGTAAATAGTCCGTTTGGTGGCTCTA 1404
QY 495 ArgProValSerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyr 514
Db |||||||
1405 CGCAATGTCAAGGCATCG-----CCAAATAGTCTTGGCAACATTGCATCGATAGATAT 1458
QY 515 ProValLysVal 518
Db |||||||
1459 CCGGTTAAATTT 1470

Search completed: February 19, 2003, 10:53:40
Job time : 110 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 09:12:57 ; Search time 1710 Seconds
(without alignments)
4924.943 Million cell updates/sec

Title: US-09-883-797-2
Perfect score: 2680
Sequence: 1 MDRERLTAEMAFROSSAVI.....EMTGNWAGSIDQYPKVYQ 520

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09883797/runat_14022003_102501_19515/app_query.fasta_1.711
-DB=EST -OPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09883797.ecgn_1_1_2874_@runat_14022003_102501_19515 -NCPH=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_estl: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_nam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1505	56.2	1981	11	AY109713	AY109713 Zea mays
2	1092	40.7	1496	11	AY108343	AY108343 Zea mays
3	1031	38.5	735	12	BG599761	BG599761 EST04656
4	1024	38.2	800	12	BG646966	BG646966 EST08585
5	1006.5	37.6	867	13	BI949576	BI949576 HVSME1001
6	997	37.2	840	10	BE055710	BE055710 GA_Ea003
7	996.5	37.2	915	14	BQ510080	BQ510080 EST617495
8	987.5	36.8	958	12	BG444087	BG444087 GA_Ea002
9	970.5	36.2	864	12	BG444393	BG444393 GA_Ea002
10	960	35.8	663	14	BQ405604	BQ405604 GA_Ed008
11	939	35.0	671	13	BQ281418	BQ281418 BJ281418
12	939	35.0	765	14	BQ989474	BQ989474 QGF17M08
13	937.5	35.0	754	13	BM112516	BM112516 EST560052
14	928	34.6	755	14	BQ872186	BQ872186 QG113006
15	927	34.5	738	12	BG586676	BG586676 EST488444
16	925	34.5	684	9	AL505481	AL505481 AL505481
17	923	34.4	722	14	BU012426	BU012426 QGJ1008.Y
18	906.5	33.8	680	14	BQ407349	BQ407349 GA_Ed010
19	906	33.8	770	14	BQ855453	BQ855453 QGB26K03
20	906	33.8	814	17	BH664493	BH664493 BOMPA49TF
21	905	33.8	634	14	BQ245540	BQ245540 TaEI5023D
22	890	33.2	642	13	BQ302152	BQ302152 BJ302152
23	887	33.1	715	12	BG128306	BG128306 EST473952
24	887	33.1	830	10	BE642615	BE642615 Cr12.6.11
25	886	33.1	753	12	BG123587	BG123587 EST469233
26	883.5	33.0	699	9	AJ497664	AJ497664 AJ497664
27	883	32.9	715	14	BQ931166	BQ931166 QGF27M06
28	880	32.8	745	17	BH685156	BH685156 BOMMW34TF
29	879	32.8	821	17	BH693376	BH693376 BOHUS43TR
30	878.5	32.8	692	14	BQ403143	BQ403143 GA_Ed005
31	874.5	32.6	912	12	BG837722	BG837722 Zm10.05c0
32	869	32.4	629	14	BQ801648	BQ801648 WHE2816_H
33	869	32.4	685	12	BG443505	BG443505 GA_Ea002
34	868.5	32.4	750	17	BH490415	BH490415 BOCBR78TF
35	867	32.4	717	12	BG124000	BG124000 EST469646
36	863	32.2	705	12	BG266005	BG266005 HVSMEa001
37	861	32.1	693	12	BG441374	BG441374 GA_Ea001
38	859	32.1	612	14	Z26005	Z26005 ATTS1282.Gr
39	859	32.1	745	12	BG128875	BG128875 EST474521
40	858.5	32.0	661	14	BQ148102	BQ148102 NF058602F
41	855	31.9	675	12	BG635850	BG635850 NF040G12D
42	854.5	31.9	669	14	BQ407360	BQ407360 GA_Ed010
43	845	31.5	602	12	BF255395	BF255395 HVSMEF000
44	844	31.5	658	14	BQ407823	BQ407823 GA_Ed000
45	844	31.5	692	14	BQ863367	BQ863367 QGC223L01

ALIGNMENTS

RESULT 1
AY109713
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY109713
Zea mays
AY109713
AY109713.1
HTC.
Zea mays.
Zea mays

1981 bp
mRNA
linear
HTC 25-MAY-2002
CL1191_1 mRNA sequence.
GI:21213540

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 1981)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.


```

FEATURES
  Location/Qualifiers
    1..735
      /organism="Solanum tuberosum"
      /cultivar="Kennebec"
      /db_xref="taxon:4113"
      /clone_lib="cSTS"
      /dev_stage="12-14 weeks post harvest"
      /tissue_type="sprouting eyes from tubers"
      /lab_host="SOLR"
      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
BASE COUNT 193 a 142 c 173 g 227 t
ORIGIN
Alignment Scores:
  Pred. No.: 2,47e-116 Length: 735
  Score: 1031.00 Matches: 188
  Percent Similarity: 90.57% Conservativeness: 33
  Best Local Similarity: 77.05% Mismatches: 23
  Query Match: 38.47% Indels: 0
  DB: 12 Gaps: 0
US-09-883-797-2 (1-520) x BG599761 (1-735)
QY 225 SerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsn 244
Db 4 TCCTTGTCCGGATGATTGTTAATCATATTAACCTTAGGGGAATGCTTTAGTACAAAT 63
QY 245 LeuGlyGlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeu 264
Db 64 CTTGGTGGATGGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 123
QY 265 LysAlaAsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrp 284
Db 124 CAAGTCCATCCACACACTATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 183
QY 285 TyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAla 304
Db 184 TATTTGGTAAATGAGAAATCCATGCTCCCTCCGAAATGTTTATTCGGATGGTGGT 243
QY 305 AlaIleLeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuValAsn 324
Db 244 GCTGTGTGTCTCAATTAACAGATCTGTATGAGAAACGATCAAAAGTACCAGCTGGTCCAT 303
QY 325 ValValArgThrHisLysGlySerAspLysAsnTyrAsnCysValTyrGlnLysGlu 344
Db 304 ACTGTTAGAACTCACAAGGCTCTGATGATAAGTCTTCACATGTGTATACCAATGGAA 363
QY 345 AspGluArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAsp 364
Db 364 GATTCGGATGGAAGGAGGCTCTCTCTGTCAAAAGAGCTAATGCGAGTAGTGGCGAT 423
QY 365 AlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeu 384
Db 424 GCTCTGAAGACAAACATCACACATTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 483
QY 385 MetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIle 404
Db 484 CTTTTCCTCCGACATTTGGTGGGAAGAGCTATTGAAGCGGAAGATAAGGCCCTATATC 543
QY 405 ProAspPheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeu 424
Db 544 CCTGATTTTAAAGTTAGCATTTGAGCATTTCTGCAATTCATGCTGGTGAAGAGCTGATCTG 603
QY 425 AspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMetThr 444
Db 604 GATGAACCTAGAGAAACCTTCAGCTCTCTGATTTGGCATATGGAGCCTTCACGAATGACA 663

```

```

QY 445 LeuHisArgPheGlyAsnThrSerSerSerLeuTyrTyrGluMetAlaTyrThrGlu 464
Db 664 CTTTCATCGATTGGACACACTTCACAGCAGCTCCCTTTGGTACGAATGGCTATTTCGAA 723
QY 465 AlaLysGlyArg 468
Db 724 GCCAAGGGTAGG 735
RESULT 4
BG646966
LOCUS
DEFINITION
  EST508585 HOGA Medicago truncatula cDNA clone pHOGA-15E18 5' end,
  mRNA sequence.
ACCESSION
  BG646966
VERSION
  BG646966.1 GI:13782078
KEYWORDS
  EST.
SOURCE
  barrel medic.
ORGANISM
  Medicago truncatula
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
REFERENCE
  1 (Bases 1 to 800)
  Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
  Utterback,T., Cho,J. and Fraser,C.M.
  ESTs from roots of Medicago truncatula treated with
  oligogalacturonides of DP 6-20
  Unpublished (2001)
  CONTACT: Michael G. Hahn
  Complex Carbohydrate Research Center
  University of Georgia
  220 Riverbend Road, Athens, GA 30602-4712, USA
  Tel: 706-542-4457
  Fax: 706-542-4412
  Email: hahn@ccrc.uga.edu
  G390572e TIGR sequence name: MTMBT33TK More information is
  available at: www.medicago.org
  Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
  Location/Qualifiers
    1..800
      /organism="Medicago truncatula"
      /cultivar="A17"
      /db_xref="taxon:3880"
      /clone="pHOGA-15E18"
      /clone_lib="HOGA"
      /tissue_type="3 day old seedling roots"
      /dev_stage="24 hours after treatment in the dark at 26 C
      with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
      presence of 100 ug/ml Gentamicin"
      /lab_host="XLOLR"
      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in SOLR cells."
BASE COUNT 242 a 157 c 177 g 224 t
ORIGIN
Alignment Scores:
  Pred. No.: 2,09e-115 Length: 800
  Score: 1024.00 Matches: 193
  Percent Similarity: 88.64% Conservativeness: 41
  Best Local Similarity: 73.11% Mismatches: 29
  Query Match: 38.21% Indels: 2
  DB: 12 Gaps: 0
US-09-883-797-2 (1-520) x BG646966 (1-800)
QY 176 ProProLysLeuAsn-MetSerGluAlaArgAlaGluAlaValMetPheGlyAl 195
Db 11 CCACAAATCCATGTTATGCTGTAAGCAAGAAAGCTGAAGAGTTATGTTGTGTC 70

```

QY 195 aleuAspSerLeuPheGluLysThrGlyLleLysProAlaGluValGlyLeuIleLeu 215
 Db 71 TATTGATGAGGTTCTCAAAAACCTGGTGAAGGCTAAGATATTGGGATTTTGGTTGT 130
 QY 215 lasnCysSerLeuPheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLy 235
 Db 131 GAATTGTAGTTGTTTAAATCCAAACCATCTCTTCTGCGCATGATTGTGAATCATATAA 190
 QY 235 smetArgGluAspLleLysSerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeu 255
 Db 191 GTTGAGAGAAATATCTTGAAGTATAATCTTGGTGGTATGGTGTAGTGGTCTTAT 250
 QY 255 eSerIleAspLeuAlaAsnAsnLeuLysAlaAsnProAsnSerTyrAlaValValVa 275
 Db 251 CTCTATTGACCTGCCAACACCTCTACAGTAGCATCCAACTCATATGCGCTTAGTAGT 310
 QY 275 lSerThrGluAsnLleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCy 295
 Db 311 GAGCATGGAGAACATAACACTAAACTGCTATTTCGGCAACGACACATCAATCTAGTGCC 370
 QY 295 sasnCysLlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspAr 315
 Db 371 AAATGTGCTCTTTAGAAATGGAGAGGAGCAGCAGTCTCTCTCCAAACAGCCACGCGCG 430
 QY 315 gLysLysSerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLy 335
 Db 431 CCTCCGATCAAAATACCAACTAGTCCACACCGCTCGAAGCAGCAAAAGGTGCAGAACAA 490
 QY 335 sasNtyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAl 355
 Db 491 ATCCTAGCGGTGCTCTTTCAAGAAGAAGACGACACAAAGCAAGTCGGTGTATCACTCTC 550
 QY 355 aArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnLleThrLeuGlyPr 375
 Db 551 AAAAGACCTAATGGCTGTCCGAGAGAGCACTCAAAACAAACATCAACATTAGGACC 610
 QY 375 oMetValLeuProLeuSerGluGlnLeuMetPheLeuLysLeuLysAspArgLysMe 395
 Db 611 ATTAGTCTACCTATGTCCGAACAGCTCTATTTCGGGACATTTGGTTCGCGCAAAAT 670
 QY 395 tPheLysLeuLysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCy 415
 Db 671 CTTCAAGATGAATAAATCAACATACATCTCTGATTTTAAATAGCTTTTGAGCATTTTG 730
 QY 415 sIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAs 435
 Db 731 TATTTCATGCTGTGTGAAGAGCCTGTTTGGATGAGTTGGAGAA-AATCTTGATTTAAGTGA 789
 QY 435 pTrpHisMet 438
 Db 790 TTGGCATATG 799
 RESULT 5
 B1949576
 LOCUS B1949576 867 bp mRNA linear EST 19-OCT-2001
 DEFINITION HVSME10014L13f Hordeum vulgare spike EST library HVCDA0012
 (Fusarium infected) Hordeum vulgare cDNA clone HVSME10014L13f, mRNA
 sequence.
 ACCESSION B1949576
 VERSION B1949576.1 GI:16290960
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 867)
 AUTHORS Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen
 , S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
 Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
 , D.
 TITLE Development of a genetically and physically anchored EST resource

JOURNAL
COMMENT

for barley genomics: Fusarium infected Morex spike cDNA library
 Unpublished (2001)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hq bases = 555
 Seq primer: AATTAAACCTCACTAAAGGG
 High quality sequence stop: 610.
 Location/Qualifiers

FEATURES
source

1. 867
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSME10014L13f"
 /clone_lib="Hordeum vulgare spike EST library HVCDA0012
 (Fusarium infected)"
 /tissue_type="Spike"
 /lab_host="TJC121"
 /note="Vector: pBluescript SK(-); Site1: EcoRI; Site2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT
ORIGIN

200 a 223 c 260 g 182 t 2 others

Alignment Scores:

Pred. No.: 3.48e-113 Length: 867
 Score: 1006.50 Matches: 199
 Percent Similarity: 86.27% Conservative: 46
 Best Local Similarity: 70.07% Mismatches: 39
 Query Match: 37.56% Indels: 5
 DB: 13 Gaps: 0

US-09-883-797-2 (1-520) x B1949576 (1-867)

QY 220 PheAsnProThrProSerLeuSerAlaMetIleValAsnHisTyrLysMetArgGluAsp 239
 Db 2 TTCAACCCGAGCCGCTCACTGTCGCCCATGGGTGGTGAACATTACAGCTGAGAGGGA 61
 QY 240 IleLysSerTyrAsnLeuGlyGlyMetGlyCysSerAlaGlyLeuLysSerIleAspLeu 259
 Db 62 ATAATCAGCTACATCTGGGAGGAATGGGGTGCAGTCCGGGCTCTTGTCCATAGATCTG 121
 QY 260 AlaAsnAsnLeuLysAlaAsnProAsnSerTyrAlaValValSerThrGluAsn 279
 Db 122 GCCAAGGATTGCTTCAAGTGCATCCCACTCGTAGCCATGCTGTGTGTGACCGAGAAC 181

280	ilThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCysIlePhe	299
Qy		
Db		
182	ATTACCTCAATTGGTATTTTGGGAACAACCGGTGCGATGCTGCTGCAATTGCGTGTTC	241
Qy		
Db		
300	ArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgArgGlnAspArgIlySerLys	319
Qy		
Db		
242	CGGATGGGTGCGCTCGCATCTGCTGCGAACAGCGGTGACAGAGGAGGAGGTCCAAG	301
Qy		
Db		
320	TyrSerLeuLeuAsnValValArgThrHisLysGlySerAspAspLysAsnTrpAsnCys	339
Qy		
Db		
302	TACGAGCTGGTACACACCGTGAGAACTCACAGGGTGCAGATGACAAGTGCCTTCAGCTGT	361
Qy		
Db		
340	ValTyrGlnLysGlnAspGluArgGlyThrIleGlyValSerLeuLeuAlaArgGluLeuMet	359
Qy		
Db		
362	GTACCCAGGAGGAGGATGACAGTGCAGAGGTGGCGTGCACATGCCAAGGACCTCATG	421
Qy		
Db		
360	SerValAlaGlyAspAlaLeuLysThrAsnIleThrThrLeuGlyProMetValLeuPro	379
Qy		
Db		
422	GGGGTGGCTGGGGATCGCTCAAGACGACATCACACGGTTGGCGCGCTGTGTGCCCA	481
Qy		
Db		
380	LeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLysLeuLys	399
Qy		
Db		
482	TTCTCGGACAGCTGCTGTTCATGGTGCACATTTGGTGGCAAGAGGTGTTCAAGATGAAG	541
Qy		
Db		
400	ValLysProTyrIleProaspPheLysLeuAlaPhecluHisPheCysIleHisAlaGly	419
Qy		
Db		
542	ATCAAGCCATACATTCCTGACTTCAAGCTGGCATTCGAGCACCTTCGCATCCACGCTGGT	601
Qy		
Db		
420	GlyArgAlaValLeuAspGluValGlnLysAsnLeuLeuAspLeuLysAspTrpHisMetGlu	439
Qy		
Db		
602	GGCGCGCTGCTGTGATGAGATAGAGAAGAC-ATGGACCTCACCGATTGGCACATGGAG	660
Qy		
Db		
440	ProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerSerLeuTrpTyrGlu	459
Qy		
Db		
661	CCGTCCTCGGGTGACTCTCTTCCG-TTGGCAACACGTCACACGCTCGGTGTGTGACAGC	719
Qy		
Db		
460	MetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnIleAla	479
Qy		
Db		
720	TGGCTTACAGGACCA-CAAGGGAGGACCCAGGAGCGGTGCAGGGTATGSCAATA-GCG	777
Qy		
Db		
480	PheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProValSerThr	499
Qy		
Db		
778	NTCGGCTCGGGGTCAA-TGTACAAGCGCCCTCTGGACGGCCTGAGCTANAGTACCCACG	836
Qy		
Db		
500	GluGluMetThr	503
Qy		
Db		
837	AAGGACGAACA	848
Qy		
Db		
RESULT 6		
BE055710	840 bp	linear EST 07-MAR-2001
LOCUS	GA_Ea0035J01f Gossypium arboreum 7-10 dpa fiber library Gossypium	
DEFINITION	arboreum cDNA clone GA_Ea0035J01f, mRNA sequence.	
ACCESSION	BE055710	
VERSION	BE055710.2	GI:13246847
KEYWORDS	EST.	
SOURCE	Gossypium arboreum.	
ORGANISM	Gossypium arboreum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
TITLE	Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.	
JOURNAL	1 (bases 1 to 840)	
COMMENT	Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry	
	D., Wood, T.C., Leslie, A. and Watkins, T.A.	
	An integrated analysis of the genetics, development, and evolution	
	of the cotton fiber	
	Unpublished (2000)	
	On Jun 8, 2000 this sequence version replaced gi:8382767.	
	Contact: Wing RA	
	Clemson University Genomics Institute	
	Clemson University	
	100 Jordan Hall, Clemson, SC 29634, USA	
	Tel: 864 656 7288	

```

QY 424 euAspGluValGlnLysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMet 444
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 TTGATGAACGTGGAGAAATTTGACGCTCTCCGAATGCATATGGAACATTCAAATGA 720
QY 444 hrLeuHisArgPheGlyAsnThrSerSerSerLeuTrpTyrGluMetAlaTyrThrG 464
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 CTCTCTT-CGAATTGGAAAA--CCTCAAGCAGTCTCTGGGTATGAATGGCTATCCGG 776
QY 464 luAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGlnLeuAlaPheGlySerGlyP 484
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 777 GAGCTTAGGGGAGGATTAGGAAGGAA-CGAACCTGGCAAAA-GCATTGGTCTCGGAT 834
QY 484 helys 485
|||||
Db 835 TCAAA 839

RESULT 7
BQ510080
LOCUS
DEFINITION
EST617495 Generation of a set of potato cDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum cDNA clone STMHH64
3' end, mRNA sequence.
ACCESSION BQ510080
VERSION BQ510080.2 GI:21925787
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusteroids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 915)
Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.
Generation of a set of potato cDNA clones for microarray analyses
unpublished (2002)
On Jun 10, 2002 this sequence version replaced gi:21368949.
Other ESTs: EST617494
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@ig.rockefeller.edu
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: 77.
FEATURES
source
Location/Qualifiers
1..915
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjete"
/db_xref="taxon:4113"
/clone="STMHH64"
/clone.lib="Generation of a set of potato cDNA clones for
microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLU"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
of tubers, or roots."
BASE COUNT 234 a 158 c 238 g 285 t
ORIGIN

Alignment Scores:
Pred. No.: 6.57e-112 Length: 915
Score: 996.50 Matches: 182
Percent Similarity: 80.86% Conservative: 63
Best Local Similarity: 60.07% Mismatches: 56
Query Match: 37.18% Indels: 2
DB: 14 Gaps: 1

US-09-883-797-2 (1-520) x BQ510080 (1-915)

```

```

QY 133 AspSerPheLeuThrMetThrGluGluAsnGlySerPheThrAspAspThrValGlnPhe 152
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 GAACGGTTTCATGACGACATTCACGGCTCACCGGTGATTTTGATGATCGCTCGCTTGGATT 66
QY 153 GlnGlnArgIleSerAsnArgAlaGlyLeuGlyAspGluThrTyrLeuProArgGlyIle 172
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 CAGAGGAAGATTCTGGAACGCTTCGGCTCGGGACCAAACTTATGTCCTCCCTGAGGCTATG 126
QY 173 ThrSerThrProLysLeuAsnMetSerGluAlaArgAlaGluAlaGluValMet 192
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 CATCAGCTTCTCCGAGCCTTCTATGAGGTCGAGGGAGAGGCTGAGCAAGTTATG 186
QY 193 PheGlyAlaLeuAspSerLeuPheGluLysThrGlyIleLysProAlaGluValGlyIle 212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 TTTGGTGCATCGACAAATTTGTTGCTAATACCTCTGTGAACCTAGAAAATAGGTGTG 246
QY 213 LeuLeuValAsnCysSerLeuPheAsnProThrProSerLeuSerAlaMetIleValAsn 232
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 CTGTGTTGAAATGTAGTTTGTTCATCCGACTCCATCGCTTTCAGCTATGATTGTGAAC 306
QY 233 HisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGlyMetGlyCysSerAla 252
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 AAGTATAAGTTGAGAGGTATATAAGAGTTTAACTCTGGAGGTATGGGTTGTAGTCT 366
QY 253 GlyLeuLeuSerIleAspLeuAlaAsnLeuLysAlaAsnProAsnSerTyrAla 272
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 367 GGTGTAATTCGCGTTGATCTTGCCAAAGGACATGTTGCAAGTCGACACAAATACCTATGCT 426
QY 273 ValValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspSerMet 292
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 427 GTTGTGTTAGTACTGAGAATATATTACTCAGAACTGTTATTTGGGATAAGAAGTCCATG 486
QY 293 LeuLeuCysAsnCysIlePheArgMetGlyGlyAlaIleLeuLeuSerAsnArgArg 312
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 487 TTGATACCAAAATGTTGTTTAGAGTCGGAGGTTCTGCTGCTCTCTATAAGTCT 546
QY 313 GlnAspArgLysLysSerLysTyrSerLeuValAsnValValArgThrHisLysGlySer 332
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 547 ATGGATAGAAGAAAGGCGAAATATAAGCTTTGTCATGCTGTTAGGACACATCGTGGGCT 606
QY 333 AspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyVal 352
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 607 CATGATAGGCATTTCTGTTGTTTACCAGAACACAGATGATCTGGGAAACTGGGGTT 666
QY 353 SerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrThr 372
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 667 TCTTTGTCAAAAGATCTCATGCAATCGCTGGGGAGCGCTTTAGACGAATATTACTACA 726
QY 373 LeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuLeuSerLeuValLys 392
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 727 TTGGTCTCTGTTGTTCTACCCATCAGTGAGCAGCTTCTGTTCTTCTCTCTGTAATC 786
QY 393 ArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLysLeuAlaPheGlu 412
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 787 AAGAAAATATTATAACCATATCAAGCTTACATCTCCAGATTTCAAGTTGGCTTTGAT 846
QY 413 HisPheCysIleHisAlaGlyClyArgAla----ValLeuAspGluVal-GlnLysAsnLe 431
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 847 CATTTCTGCATACACGCTGGGTGGGAAGGCTGGTATTATTGACGAGCTGGGAAAGAAATTT 906
QY 431 uAspLeu 433
|||||
Db 907 ACAGCTG 913

RESULT 8
BG444087
LOCUS
DEFINITION GA_Ea0023E01f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboresum cDNA clone GA_Ea0023E01f, mRNA sequence.
ACCESSION BG444087
VERSION BG444087.1 GI:13353739
KEYWORDS EST.

```


BASE COUNT 250 a 209 c 190 g 215 t
ORIGIN

Alignment Scores:

Pred. No.: 9,78e-109 Length: 864
Score: 970.50 Matches: 174
Percent Similarity: 88.70% Conservative: 38
Best Local Similarity: 72.80% Mismatches: 26
Query Match: 36.21% Indels: 1
DB: 12 Gaps: 1

US-09-883-797-2 (1-520) x BQ444393 (1-864)

Qy 278 GluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCys 297
Db 3 GAGAACATTACTCTCAACTGGGACTTCGGCAACGACCGATCCATGCTACTGCTCAACTGC 62
Qy 298 IlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLys 317
Db 63 TTGTTCCGATGGGGGGTGGCGGATCTTCTATCAAAACCGGTCTATCCGATCGCGCGCG 122
Qy 318 SerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyr 337
Db 123 TCCAAGTACCAACTCATCCACCGTACGAAACCCACAAGAGCGCCGACACAAATGCTAC 182
Qy 338 AsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGlu 357
Db 183 AACTGCGCTTCCCAACGTGAGCAGCAGCACCAACAAATAGGCGTTTCCCTCTCCAAAGAC 242
Qy 358 LeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetVal 377
Db 243 CTCATGGCGTGGCGGAGGAGCCCTCAAAACCAACATCACACCCCTCGGTCCATTAGTC 302
Qy 378 LeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLys 397
Db 303 CTCGCCATGCGGAAACAACTCTCTTTTCATCACTTTAGTACCCGAAAGCTCTCAA 362
Qy 398 LeuLysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHis 417
Db 363 ATGAGATCAGGCCATACATCCCGGATTTCAAACTAGCTTTTCGAGCATTTTTCATCCT 422
Qy 418 AlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHis 437
Db 423 GCAGGTGGGAGACCGGTGTAGTAGCTAGACCTAGAAAGAACCTTGAGCTTCAGATTGGC 482
Qy 438 MetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerLeuTrp 457
Db 483 ATGGAACCATCGAGGATGACACTTTACAGGTTCCGTTAACAGCTCGAGCAGCTCTTATGG 542
Qy 458 TyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGln 477
Db 543 TACGAACCTAGCTTACTCGGAAGGCCAAAGGAAGGATCCGAAAGGTGATCGGACATGGC 602
Qy 478 IleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProVal 497
Db 603 ATTGCATTGGGTCAGGTTTAATGCAACAGTCTGCTATGGAAGCATTTGAAGACCAT 662
Qy 498 SerThrGluGluMetThrGlyAsnAlaTrpAlaGlySerIleAspGlnTyrProVal 516
Db 663 AATCCAGCAAG---GAGAAGAGTCCATGGATTGATGAATGATGATGCTGCTT 716

RESULT 10

BQ405604

LOCUS BQ405604 663 bp mRNA linear EST 22-MAY-2002
DEFINITION GA_Ed0084G03f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ed0084G03f, mRNA sequence.

ACCESSION BQ405604

VERSION BQ405604.1

KEYWORDS EST

SOURCE Gossypium arboreum.

ORGANISM

Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS

Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)

JOURNAL

COMMENT

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 559
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 652.
Location/Qualifiers

FEATURES

source

1..663
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ed0084G03f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 186 a 169 c 150 g 157 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 1.25e-107 Length: 663
Score: 960.00 Matches: 169
Percent Similarity: 91.82% Conservative: 33
Best Local Similarity: 76.82% Mismatches: 18
Query Match: 35.82% Indels: 0
DB: 14 Gaps: 0

US-09-883-797-2 (1-520) x BQ405604 (1-663)

Qy 278 GluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArgSerMetLeuLeuCysAsnCys 297
Db 2 GAGAACATTACTCTCAACTGGTACTTCGGCAACGACCGATCTATGCTCTCAAAATGC 61
Qy 298 IlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsnArgGlnAspArgLysLys 317
Db 62 CTCCTCCGATGGGGGTGGCGCAATCTCTCTCCAAACCGCTCATCCGATCGCACCGC 121
Qy 318 SerLysTyrSerLeuValAsnValValArgThrHisLysGlySerAspAspLysAsnTyr 337
Db 122 TCCAATACCAACTCATTCACACCGTACGACGACGACAAAGGTGCGCATGACAAATGCTAC 181
Qy 338 AsnCysValTyrGlnLysGluAspGluArgGlyThrIleGlyValSerLeuAlaArgGlu 357
Db 182 AACTGCGCTTCCCAAGTGGAGCAGCACCAAAAGATCGCATTTCCCTCTCGAAAGAC 241
Qy 358 LeuMetSerValAlaGlyAspAlaLeuLysThrAsnIleThrLeuGlyProMetVal 377
Db 242 CTCATGGCTGTCGGGAGAGCCCTTAAACCAACATCACCACTCTGGGCGCACATGTT 301
Qy 378 LeuProLeuSerGluGlnLeuMetPheLeuIleSerLeuValLysArgLysMetPheLys 397
Db 302 CTCCTCATGTCGGAGCAACTCTGTTTTTCGTCACCTTGGTGGCAAGAAAGTGTGAAG 361
Qy 398 LeuLysValLysProTyrIleProAspPheLysLeuAlaPheGluHisPheCysIleHis 417
Db 362 ATGAAGATCAAAACCTATATCCAGATTTCAGATTGGCATTCGCAATTTTGCATTCAT 421
Qy 418 AlaGlyGlyArgAlaValLeuAspGluValGlnLysAsnLeuAspLeuLysAspTrpHis 437
Db 422 GCAGGTGGGAGGCGGTGCTAGATGAGCTTGAAGAAACCTTGACCTTACAGCTTGGCAC 481

Rosidae; eursoids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 663)

QY	438	MetGluProSerArgMetThrLeuHisArgPheGlyAsnThrSerSerSerLeuTrp	457		9	GGGTGCAGTGCCGGGCTCTCTCCATAGATCTGGCCNAGGATTTGCTCCAGGTGCACCCC	68
Db	482	ATGGACCATCGAATGAGCGCTTTACAGATTTGGAAACACTTCAAGCAGTCTTTGTGG	541		269	AsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsn	288
QY	458	TyrGluMetAlaTyrThrGluAlaLysGlyArgValLysAlaGlyAspArgLeuTrpGln	477		69	AACTCGTATGCAATGGTGTGTCAGCAGGAGAACATTAACCTGAATTTGGTAATTTGGGAAC	128
Db	542	TATGAATTAGCTTACTGTAAGCCAAAGGAAGATCAAGAGGGGTGATAAGACATGGGCAG	601		289	AspArgSerMetLeuLeuCyAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeu	308
QY	478	IleAlaPheGlySerGlyPheLysCysAsnSerAlaValTrpLysAlaLeuArgProVal	497		129	AACCGGTGATGCTGTGCTCAAAATTCCTGTTCCGATGGCTGCCTGCATCTCTCTG	188
Db	602	ATTGCTTCGGGTGAGGATTAAGTGCACAGTGCANGTTGGAAGGCATTTGAAGACCATC	661		309	SerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValAlaArgThr	328
RESULT 11					189	TCGAACAAGCGGTGACAGAGGAGGAGTCAAGTAGCTGACACATCTGTAGGACT	248
BJ281418					329	HisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGly	348
LOCUS					249	CACAAGGTGTCAGATGACAAGTCTTCACCTGTGTCCACAGGAGGAGGATGATAGCGC	308
DEFINITION					349	ThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThr	368
ACCESSION					309	AAGTTGGCGTGGCAGTATCAAGGACCTCATGGCGGTGGCTGGGATGGCTCAAGACG	368
VERSION					369	AsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIle	388
KEYWORDS					369	AACATCAACAGCTTGGCCGCTTGTGTACCATTTCTCGGAGCAGCTGCTTTCATGCTC	428
SOURCE					389	SerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLys	408
ORGANISM					429	ACATTTGGTGGCAAGAGCTGTTCAAGATGAAGATCAAGCATCATCTCTGACTTCAAG	488
REFERENCE					409	LeuAlaPheGluHisPheCysIleHisAlaGlyArgAlaValLeuAspGluValGln	428
AUTHORS					489	CTGGCATTCGAGCACTTCTGCATCCACGCTGGTGGCGGCTGTGTGTATGATAGATAG	548
TITLE					429	LysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPhe	448
JOURNAL					549	AAGAATCATGGACCTCACCACTGGCAGTGGAGCCGCTCCGAGTACTCTCTCCGGTTC	608
COMMENT					449	GlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArg	468
FEATURES					609	GGCAACACCTCCAGCAGCTCGCTCTGTGTAGAGCTGGCTACAGCGGAGGAGGAGG	668
source					QY	469	Val 469
					Db	669	ATC 671
					RESULT 12		
					BO989474		
					LOCUS		
					DEFINITION		
					ACCESSION		
					VERSION		
					KEYWORDS		
					SOURCE		
					ORGANISM		
					REFERENCE		
					AUTHORS		
					TITLE		
					JOURNAL		
					COMMENT		
					BASE COUNT		
					ORIGIN		
					Alignment Scores:		
					Pred. No.:		
					Score:		
					Percent Similarity:		
					Best Local Similarity:		
					Query Match:		
					DB:		
					US-09-883-797-2 (1-520) x BJ281418 (1-671)		
QY	249	GlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeuLysAlaAsnPro	268		9	GGGTGCAGTGCCGGGCTCTCTCCATAGATCTGGCCNAGGATTTGCTCCAGGTGCACCCC	68
					269	AsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsn	288
					69	AACTCGTATGCAATGGTGTGTCAGCAGGAGAACATTAACCTGAATTTGGTAATTTGGGAAC	128
					289	AspArgSerMetLeuLeuCyAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeu	308
					129	AACCGGTGATGCTGTGCTCAAAATTCCTGTTCCGATGGCTGCCTGCATCTCTCTG	188
					309	SerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValAlaArgThr	328
					189	TCGAACAAGCGGTGACAGAGGAGGAGTCAAGTAGCTGACACATCTGTAGGACT	248
					329	HisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGly	348
					249	CACAAGGTGTCAGATGACAAGTCTTCACCTGTGTCCACAGGAGGAGGATGATAGCGC	308
					349	ThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThr	368
					309	AAGTTGGCGTGGCAGTATCAAGGACCTCATGGCGGTGGCTGGGATGGCTCAAGACG	368
					369	AsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIle	388
					369	AACATCAACAGCTTGGCCGCTTGTGTACCATTTCTCGGAGCAGCTGCTTTCATGCTC	428
					389	SerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLys	408
					429	ACATTTGGTGGCAAGAGCTGTTCAAGATGAAGATCAAGCATCATCTCTGACTTCAAG	488
					409	LeuAlaPheGluHisPheCysIleHisAlaGlyArgAlaValLeuAspGluValGln	428
					489	CTGGCATTCGAGCACTTCTGCATCCACGCTGGTGGCGGCTGTGTGTATGATAGATAG	548
					429	LysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPhe	448
					549	AAGAATCATGGACCTCACCACTGGCAGTGGAGCCGCTCCGAGTACTCTCTCCGGTTC	608
					449	GlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArg	468
					609	GGCAACACCTCCAGCAGCTCGCTCTGTGTAGAGCTGGCTACAGCGGAGGAGGAGG	668
					QY	469	Val 469
					Db	669	ATC 671
					RESULT 12		
					BO989474		
					LOCUS		
					DEFINITION		
					ACCESSION		
					VERSION		
					KEYWORDS		
					SOURCE		
					ORGANISM		
					REFERENCE		
					AUTHORS		
					TITLE		
					JOURNAL		
					COMMENT		
					BASE COUNT		
					ORIGIN		
					Alignment Scores:		
					Pred. No.:		
					Score:		
					Percent Similarity:		
					Best Local Similarity:		
					Query Match:		
					DB:		
					US-09-883-797-2 (1-520) x BJ281418 (1-671)		
QY	249	GlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeuLysAlaAsnPro	268		9	GGGTGCAGTGCCGGGCTCTCTCCATAGATCTGGCCNAGGATTTGCTCCAGGTGCACCCC	68
					269	AsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsn	288
					69	AACTCGTATGCAATGGTGTGTCAGCAGGAGAACATTAACCTGAATTTGGTAATTTGGGAAC	128
					289	AspArgSerMetLeuLeuCyAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeu	308
					129	AACCGGTGATGCTGTGCTCAAAATTCCTGTTCCGATGGCTGCCTGCATCTCTCTG	188
					309	SerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValAlaArgThr	328
					189	TCGAACAAGCGGTGACAGAGGAGGAGTCAAGTAGCTGACACATCTGTAGGACT	248
					329	HisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGly	348
					249	CACAAGGTGTCAGATGACAAGTCTTCACCTGTGTCCACAGGAGGAGGATGATAGCGC	308
					349	ThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThr	368
					309	AAGTTGGCGTGGCAGTATCAAGGACCTCATGGCGGTGGCTGGGATGGCTCAAGACG	368
					369	AsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIle	388
					369	AACATCAACAGCTTGGCCGCTTGTGTACCATTTCTCGGAGCAGCTGCTTTCATGCTC	428
					389	SerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLys	408
					429	ACATTTGGTGGCAAGAGCTGTTCAAGATGAAGATCAAGCATCATCTCTGACTTCAAG	488
					409	LeuAlaPheGluHisPheCysIleHisAlaGlyArgAlaValLeuAspGluValGln	428
					489	CTGGCATTCGAGCACTTCTGCATCCACGCTGGTGGCGGCTGTGTGTATGATAGATAG	548
					429	LysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPhe	448
					549	AAGAATCATGGACCTCACCACTGGCAGTGGAGCCGCTCCGAGTACTCTCTCCGGTTC	608
					449	GlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArg	468
					609	GGCAACACCTCCAGCAGCTCGCTCTGTGTAGAGCTGGCTACAGCGGAGGAGGAGG	668
					QY	469	Val 469
					Db	669	ATC 671
					RESULT 12		
					BO989474		
					LOCUS		
					DEFINITION		
					ACCESSION		
					VERSION		
					KEYWORDS		
					SOURCE		
					ORGANISM		
					REFERENCE		
					AUTHORS		
					TITLE		
					JOURNAL		
					COMMENT		
					BASE COUNT		
					ORIGIN		
					Alignment Scores:		
					Pred. No.:		
					Score:		
					Percent Similarity:		
					Best Local Similarity:		
					Query Match:		
					DB:		
					US-09-883-797-2 (1-520) x BJ281418 (1-671)		
QY	249	GlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeuLysAlaAsnPro	268		9	GGGTGCAGTGCCGGGCTCTCTCCATAGATCTGGCCNAGGATTTGCTCCAGGTGCACCCC	68
					269	AsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsn	288
					69	AACTCGTATGCAATGGTGTGTCAGCAGGAGAACATTAACCTGAATTTGGTAATTTGGGAAC	128
					289	AspArgSerMetLeuLeuCyAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeu	308
					129	AACCGGTGATGCTGTGCTCAAAATTCCTGTTCCGATGGCTGCCTGCATCTCTCTG	188
					309	SerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValAlaArgThr	328
					189	TCGAACAAGCGGTGACAGAGGAGGAGTCAAGTAGCTGACACATCTGTAGGACT	248
					329	HisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGly	348
					249	CACAAGGTGTCAGATGACAAGTCTTCACCTGTGTCCACAGGAGGAGGATGATAGCGC	308
					349	ThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThr	368
					309	AAGTTGGCGTGGCAGTATCAAGGACCTCATGGCGGTGGCTGGGATGGCTCAAGACG	368
					369	AsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIle	388
					369	AACATCAACAGCTTGGCCGCTTGTGTACCATTTCTCGGAGCAGCTGCTTTCATGCTC	428
					389	SerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLys	408
					429	ACATTTGGTGGCAAGAGCTGTTCAAGATGAAGATCAAGCATCATCTCTGACTTCAAG	488
					409	LeuAlaPheGluHisPheCysIleHisAlaGlyArgAlaValLeuAspGluValGln	428
					489	CTGGCATTCGAGCACTTCTGCATCCACGCTGGTGGCGGCTGTGTGTATGATAGATAG	548
					429	LysAsnLeuAspLeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPhe	448
					549	AAGAATCATGGACCTCACCACTGGCAGTGGAGCCGCTCCGAGTACTCTCTCCGGTTC	608
					449	GlyAsnThrSerSerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArg	468
					609	GGCAACACCTCCAGCAGCTCGCTCTGTGTAGAGCTGGCTACAGCGGAGGAGGAGG	668
					QY	469	Val 469
					Db	669	ATC 671
					RESULT 12		
					BO989474		
					LOCUS		
					DEFINITION		
					ACCESSION		
					VERSION		
					KEYWORDS		
					SOURCE		
					ORGANISM		
					REFERENCE		
					AUTHORS		
					TITLE		
					JOURNAL		
					COMMENT		
					BASE COUNT		
					ORIGIN		
					Alignment Scores:		
					Pred. No.:		
					Score:		
					Percent Similarity:		
					Best Local Similarity:		
					Query Match:		
					DB:		
					US-09-883-797-2 (1-520) x BJ281418 (1-671)		
QY	249	GlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnAsnLeuLeuLysAlaAsnPro	268		9	GGGTGCAGTGCCGGGCTCTCTCCATAGATCTGGCCNAGGATTTGCTCCAGGTGCACCCC	68
					269	AsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsn	288
					69	AACTCGTATGCAATGGTGTGTCAGCAGGAGAACATTAACCTGAATTTGGTAATTTGGGAAC	128
					289	AspArgSerMetLeuLeuCyAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeu	308
					129	AACCGGTGATGCTGTGCTCAAAATTCCTGTTCCGATGGCTGCCTGCATCTCTCTG	188
					309	SerAsnArgArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValAlaArgThr	328
					189	TCGAACAAGCGGTGACAGAGGAGGAGTCAAGTAGCTGACACATCTGTAGGACT	248
					329	HisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGly	348
					249	CACAAGGTGTCAGATGACAAGTCTTCACCTGTGTCCACAGGAGGAGGATGATAGCGC	308
					349	ThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThr	368
					309	AAGTTGGCGTGGCAGTATCAAGGACCTCATGGCGGTGGCTGGGATGGCTCAAGACG	368
					369	AsnIleThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIle	388
					369	AACATCAACAGCTTGGCCGCTTGTGTACCATTTCTCGGAGCAGCTGCTTTCATGCTC	428


```

Db 19 ATTACACTTCAACCGGTCTAACCGGTTGATAGTGTATTTTCTACTAGGGGTGTAT 78
Qy 107 ValAlaAsnArgSerLysProValTyrLeuValAspPheSerCysTyrLysProGluAsp 126
Db 79 TA-TGTAAAAAACCTAGACCGGTTTATTGTTGATTTTGCATGTTTCAAAACCGGAAGA 137
Qy 127 GluArgLysIleSerValAspSerPheLeuThrMetThrGluGluAsnGlySerPheThr 146
Db 138 GAACGAAAAATATCTCGATTCTGTTTGAATATGACAGAAAGAAATGGTGGCTTGA 197
Qy 147 AspAspThrValGlnPheGlnArgIleSerAsnArgAlaGlyLeuGlyAspGluThr 166
Db 198 GACGAACATAGTATTTCAAAAAAGATATCTCATGTTCTGTTTAGTGACGAGACG 257
Qy 167 TyrLeuProArgGlyIleThrSerThrProLysLysLeuAsnMetSerGluAlaArgAla 186
Db 258 TATTTGCCATAAGGAATCATCATCCCAACCACTCAACATGAAAGAGCGACGTGCT 317
Qy 187 GluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyLys 206
Db 318 GAGCGGAGCGGTTATGTTGGTGCATTGATTCATTATTAGTAAACACAAATCAAG 377
Qy 207 ProAlaGluValGlyIleLeuValAsnCysSerLeuPheAsnProThrProSerLeu 226
Db 378 CCAGAGAAATTTGGAATCTTTTAGTGAATTTAGTTGTTTAAATCCCAACGCATCGCT 437
Qy 227 SerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGly 246
Db 438 TCATCAATGATTTGCAATCACTACAAAGCTCAACATGACATCAAAAGTTAATAATTAGT 497
Qy 247 GlyMetCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLysAla 266
Db 498 GGAATGGGATGATGCTGGCTTAATTTCAATTTGATTTAGCCAAACAACTATTAAAGCA 557
Qy 267 AsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPhe 286
Db 558 AATCAAAATTCATATGCTGTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 617
Qy 287 GlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetClyGlyAlaAlaIle 306
Db 618 GGAATGATAGATCAATGTTGCTATGCAATTTGATTTATTCGATGGGAGGAGCGCAATG 677
Qy 307 LeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValVal 326
Db 678 CTTTGTCTACAAAGTCGAA-GATCGACC-CGGTCTAATATGAGTTGCTTACACCGGTT 735
Qy 327 ArgThrHisLys 330
Db 736 CGAACCCATAAG 747

RESULT 14
BQ872186
LOCUS
DEFINITION
BQ872186.yg.ab1 QG-ABCD1 lettuce salinas Lactuca sativa cDNA clone
QGI13006, mRNA sequence.
ACCESSION
BQ872186
VERSION
BQ872186.1 GI:22258744
KEYWORDS
EST.
SOURCE
Lactuca sativa.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Lactuceae; Lactuceae;
Lactuca.
REFERENCE
1 (bases 1 to 755)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
unpublished (2002)

```

```

COMMENT
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4873, see http://cgdb.ucdavis.edu/
for details.
Plate: QGI13 row: 0 column: 06.
Location/Qualifiers
FEATURES
source
1..755
/organism="Lactuca sativa"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGI13006"
/clone_lib="QG-ABCD1 lettuce salinas"
/lab_host="E.Coli"
/note="vector: pBRcDNASfIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=QG-ABCD1 lettuce salinas
TAG_TISSUE=roots
TAG_SEQ=GTTCACGGG"
BASE COUNT 217 a 181 c 156 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 1.4e-103 Length: 755
Score: 928.00 Matches: 165
Percent Similarity: 86.85% Conservative: 53
Best Local Similarity: 65.74% Mismatches: 33
Query Match: 34.63% Indels: 0
DB: 14 Gaps: 0
US-09-883-797-2 (1-520) x BQ872186 (1-755)
Qy 187 GluAlaGluAlaValMetPheGlyAlaLeuAspSerLeuPheGluLysThrGlyLys 206
Db 3 GAGCGGAGCAGGTTATGTACGAGCTTTAGATAATCTGTTTCCAGTACCGAGTTAAA 62
Qy 207 ProAlaGluValGlyIleLeuValAsnCysSerLeuPheAsnProThrProSerLeu 226
Db 63 CCAAAAGACATCGGCATCTCTGTTGGTGAATGTAGTGTGTTCAATCCGACTCTTCTTG 122
Qy 227 SerAlaMetIleValAsnHisTyrLysMetArgGluAspIleLysSerTyrAsnLeuGly 246
Db 123 TCTTCCATGATCGTTAAACAAATACAAATTAAGAGGTAAACATCCGAGCTTCAATTTGGGC 182
Qy 247 GlyMetGlyCysSerAlaGlyLeuIleSerIleAspLeuAlaAsnLeuLysAla 266
Db 183 GGAATGGGATGACGCGCGGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 242
Qy 267 AsnProAsnSerTyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPhe 286
Db 243 CACCGGAATACATACCGCTGCTGTTGTCAGCACCGCAAAACATCACCAAAATTTGTTTC 302
Qy 287 GlyAsnAspArgSerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAlaIle 306
Db 303 GGAACAAAAAGTCCATGCTGATCCCAATTTGTTTATTCGATGCTGGTGGTTCGAGTT 362
Qy 307 LeuLeuSerAsnArgGlnAspArgLysLysSerLysTyrSerLeuValAsnValVal 326
Db 363 TTACTCTCAACAAATCAATTCGATAAAAGAGAGCAAAATCAAACTCGTTCATGTCGTC 422
Qy 327 ArgThrHisLysGlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGlu 346

```

```

Db 423 AGAACCCACCGTGGTCAGATGAGAAAGCTTTCCGTTCCGTATATCAAGAACACAGACGCC 482
QY 347 ArgGlyThrIleGlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeu 366
Db 483 GCCGGAAACAGTGGTCTTTATCAAAAGATCTCATGGCAATCGCGGCGGCACTG 542
QY 367 LysThrAsnIleThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPhe 386
Db 543 AAAACCAACATCACTACTCTGGGCCACTTGTCTTCCAAATCAGTGAACAGCTCCTTTTC 602
QY 387 LeuIleSerLeuValLysArgLysMetPheLysLeuLysValLysProTyrIleProAsp 406
Db 603 TTCTGCACCTTATAATAAAATCTTCAATAAACACATCAACACCTACATTCCTGAT 662
QY 407 PheLysLeuAlaPheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGlu 426
Db 663 TTCAATAGCTTTCACCATTTCTGCATCCACGCTGGTGGTGGGCTGTGATTGATGAG 722
QY 427 ValGlnLysAsnLeuAspLysAspTrpHis 437
Db 723 CTTGAGAAAGATCTGCAGCTATACCCGACACAT 755

RESULT 15
LOCUS BG586676
DEFINITION EST488444 MHAM Medicago truncatula/Glomus versiforme mixed EST
ACCESSION BG586676
VERSION BG586676.1 GI:13601740
KEYWORDS EST.
SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
ORGANISM Medicago truncatula/Glomus versiforme mixed EST library.
REFERENCE 1 (bases 1 to 738)
AUTHORS Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula after colonization with
JOURNAL Glomus versiforme, 2001
COMMENT Unpublished (2001)
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N385742e TIGR sequence name: MTD093TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES
Location/Qualifiers
1..738
/organism="Medicago truncatula/Glomus versiforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-44017"
/clone.lib="MHAM"
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_post="E. coli strain XL0LR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
200 a 97 c 185 g 256 t
BASE COUNT
ORIGIN

```

```

Alignment Scores:
Pred. No.: 1-79e-103 Length: 738
Score: 927.00 Matches: 169
Percent Similarity: 84.62% Conservative: 40
Best local Similarity: 68.42% Mismatches: 36
Query Match: 34.59% Indels: 2
DB: 12 Gaps: 1

```

US-09-883-797-2 (1-520) x BG586676 (1-738)

```

QY 271 TyrAlaValValSerThrGluAsnIleThrLeuAsnTrpTyrPheGlyAsnAspArg 290
Db 3 TATGCTGTGTGGTTAGTACTGAGAATATTACTCAAAATGGTATTGGTAAATACAAA 62
QY 291 SerMetLeuLeuCysAsnCysIlePheArgMetGlyGlyAlaAlaIleLeuLeuSerAsn 310
Db 63 TCTATGTGATTCGCAATTTGTTTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 122
QY 311 ArgArgGlnAspArgLysSerLysTyrSerLeuValAsnValValArgThrHisLys 330
Db 123 AAAGGCTGTGATAGAGCAGGCGCTAAGTATAAGCTTGTTCATCTTGTGAGGACTCATAA 182
QY 331 GlySerAspAspLysAsnTyrAsnCysValTyrGlnLysGluAspGluArgGlyThrIle 350
Db 183 GGTGCTGATGATAAAGCAATTTAAGTGTGTTTATCAAGAACAAGACCATGTTGGGAAAC 242
QY 351 GlyValSerLeuAlaArgGluLeuMetSerValAlaGlyAspAlaLeuLysThrAsnIle 370
Db 243 GGTGCTGTGCTTAAAGATCTTATGGCTATTGCTGGTGGTGGTGGTGGTGGTGGTGGT 302
QY 371 ThrThrLeuGlyProMetValLeuProLeuSerGluGlnLeuMetPheLeuIleSerLeu 390
Db 303 ACACTTTGGGTCCTCTTGTGTACCTGTGTAGTGAACAGCTTTGTTTACTACTTTG 362
QY 391 VallysArgLysMetPheLysLeuLysValLysProTyrIleProAspPheLysLeuAla 410
Db 363 GTTATTAAAGAAATGGTTTAAATCAAAAACCTAAGCCTTATATACCTGATTTTAAAGCTGCT 422
QY 411 PheGluHisPheCysIleHisAlaGlyGlyArgAlaValLeuAspGluValGlnLysAsn 430
Db 423 TTTGAGCATTTTGTATTATTCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 482
QY 431 LeuAspLeuLysAspTrpHisMetGluProSerArgMetThrLeuHisArgPheGlyAsn 450
Db 483 TTGCAGCTTATGCCTGATCATGTTGAGGCATCTAGAATGACCTTTGCATAGATTTGGCAAT 542
QY 451 ThrSerSerSerLeuTrpTyrGluMetAlaTyrThrGluAlaLysGlyArgValLys 470
Db 543 ACTTCTTCAAGTTCAATTTGCTATCAATTGCTTACATTGAAGCTTAAAGGAAGGATGAGA 602
QY 471 AlaGlyAspArgLeuTrpGlnIleAlaPheGlySerGlyPheLysCysAsnSerAlaVal 490
Db 603 AAGGAAACAGAAATTTGGCAGATTCGATTTGGGAGTGGTGGTGGTGGTGGTGGTGGTGG 662
QY 491 TrpLysAlaLeuArgProValSerThrGluGluMetThrGlyAsnAlaTrpAlaGlySer 510
Db 663 TGCAGGCTATGAACACATGTGAAGCTTCAACCTATG-----AGTCCATGGGAAGATTGC 716
QY 511 IleAspGlnTyrProValLys 517
Db 717 ATTGATAGGTATCCAGTTGAG 737

```

Search completed: February 19, 2003, 10:51:51
Job time : 1724 secs

